O'Bryen, Barbara

From: Sent:

Switzer, Juliet

Thursday, December 18, 2003 8:37 AM O'Bryen, Barbara

To: Subject:

please search

09/889491

please search seq id no 13 and 14 in all prior art databases. please also search in reg file in oligos of 100 or fewer crossed as appropriate with alignments. Thanks.

Juliet Switzer Art Unit 1634 703 306 5824 office CM1 12D15 mailbox CM1 12E12

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model Run on: December 18, 2003, 09:0217, Search time 1397,89 Seconds (without alignments) 913.763 Willion cell updates/sec Title: Scoring table: DESTITY, NUC Searched: 2889711 seqs, 20454813386 residues Total number of hits satisfying chosen paxameters: Total number of hits satisfyin	nucleic search, using
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID 1 31 100.0 2415 9 HDWSRAPO 2 31 100.0 2415 9 HDWSRAPO 3 29.4 94.8 72612 9 HDWSRAPO 4 29.4 94.8 72612 9 HDWSRAPO 5 29.4 94.8 176224 9 ACC99064 6 29.2 174.2 119519 2 ACC18613 12 23 74.2 119519 2 ACC18613 13 23 74.2 119519 2 ACC18613 14 23 74.2 119519 2 ACC18613 15 23 74.2 202233 9 ACC99864 16 23 74.2 217879 2 BX005264 ACC990664 Homo sapi 17 29.1 1244 9 ACC990664 18 23 74.2 217879 2 BX005265 19 23 74.2 229264 1 ARC18706 20 22.6 72.9 17444 8 ACC990466 21 22.6 72.9 17444 8 ACC990466 22 22.7 71.6 120000 3 ACC18706 23 22.7 71.6 23819 2 ACC98646 24 22.2 71.6 120000 3 ACC18706 25 22.7 71.6 23819 2 ACC98646 26 22.2 71.6 120000 3 ACC18707 27 22.2 71.6 23819 2 ACC98646 28 22.7 71.6 120000 3 ACC18707 28 22.7 71.6 120000 3 ACC18707 28 22.7 71.6 120000 3 ACC18707 28 22.7 71.0 120529 3 ACC1301 28 22.7 71.0 120529 2 ACC1301 29 22.7 71.0 120529 3 ACC1301 20 22.7 71.0 120549 3 ACC1301 20 22.7 71.0 120549 3 ACC1301 20 22.7 71.0 120549 3 ACC12301 20 22.7 71.0 120549 3 ACC12301

ALIGNMENTS

TITLE JOURNAL	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX028511	RESULT 1
Genetic predisposition Genetic WO 0042216-A 14 20-JUL-2000;	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Suteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1.</pre>	Homo sapiens	Homo sapiens (human)		AX028511.1 GI:10189694	AX028511	6	AX028511 31 bp DNA linear PAT 16-SEP-2000		

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ACCESSION
VERSION
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     Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1221)

1. (bases 1 to 1221)
                                                                                                                                                                                                                                                                      31,
                                                                                                                               1221 bp Homo sapiens bone sialoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 2415)
Kim,R.H., Shapiro,H.S., Li,J.J., Wrana,J.L. and Sodek
Characterization of the human bone sialoprotein (BSP)
Kerr,J.M., Pisher,L.W., Termine,J.D., Wang,M.G., McBride,O.W. and
                                                                                               sialoprotein
                                                                                                          L09554
L09554.1 GI:292488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone sialoprotein
L24756 L06823
L24756.1 GI:438617
                                                                Homo sapiens (human)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                Submitted (08-APR-2002) CIHR Group of Toronto, Room 234, 150 College (
                                                                                                                                                                                                                             2 (bases 1 to 2461)
Kiyoshima, T. and Sodek, J.
Direct Submission
                                                                                                                                                                                                                                                                                       Gene 299 (1-2), 205-217
                                                                                                                                                                                                                                                                                                      elements
                                                                                                                                                                                                                                                                                                                Kiyoshima, T., Yamauchi, M., Wong, C., Jheon, A., Ganss, B. and Sodek, J. An Li element disrupts human bone sialoprotesin promoter: lack of tissue-specific regulation by distalless (Dlx5) and runt homeodomain protein2 (Runx2)/core binding factor al (Cbfal)
                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 2461)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="IBSP"
2052. .2056
/gene="IBSP"
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                                                     /note="clone provided by CIHR Genome Facility, Hospital
for Sick Children, Toronto, ON, Canada"
                                                                                                                                                                                  o, Room 234, 150 Co.
Location/Qualifiers
                                                                                                                         organism="Homo sapiens"
mol_type="genomic DNA"
db_xref="taxon:9606"
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cell_type="fibroblast"
tissue_type="lung"
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map="4q11-q21"
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                                                                                                                 chromosome="4"
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Pred. No. 6.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1781
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                                                                                                                                                       Research, 320 Charles Street, Cambridge, MA 02141, US: All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (Dases 1 to 78036)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-PBB-2001) Whitehead Institute/MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 4, clone CTD-2363K13
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Contact: sequence submissions@genome.wi.mit.edu
                                                                                      Center code: WIBR
                                                                                                          Center: Whitehead Institute/ MIT
                                                     Web site: http://www-seq.wi.mit.edu
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Matches
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18081 ATAGTGAAAACTTGTATAATTATGAAATTTT 18051
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                                                                                                              Similarity
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Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 77262 bases at least Q40 Consensus quality: 77867 bases at least Q30 Consensus quality: 77801 bases at least Q20 Insert size: 79000; agarose-fp Insert size: 79366; sum-of-contigs Quality coverage: 8.0 in Q20 bases; sum-of-contigs Quality coverage: 8.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                       22977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
                                                                                         Conservative
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|2565, .78036
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                                                                                                                                                                                                                                                                                                                                                                 'clone="CTD-2363K13"
'clone_lib="CITD Human BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Homo sapiens"
mol_type="genomic DNA"
'db_xref="taxon:9606"
'chromosome="4"
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                                                                                                            94.8%;
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REFERENCE
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                                                                                                                                                                                                                                                                     RESULT 6
AC093768
                                                                                                                                                                                                                                       DEFINITION
                                          L (bases 1 to 187624)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99033792
                                                                                                                                                                                                187624 bp
Homo sapiens BAC clone RP11-113G13
AC093768 AC021959
AC093768.3 GI:16973767
2 (bases 1 to 187624)
Harkins, C., Kozlowicz, A.
                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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   and Doebber, A.
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                                                                                                                                                                                                                                      from 4, complete
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COMMENT
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                                                                                                                                                                                                                                    The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this
                                                                  NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is AC087106. Actual s
Clone is at base position 1 of RP11-113G13; actual end
position 187624 of RP11-113G13.
                                                                                                                                                                                                                                                                                                                                                                              SOURCE INFORMATION:
The RFCI-11 human B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                               coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sapiens@watson.wustl.edu
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NID:g11375882)"
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                                                                                                                                                                                                                                                                            AUTHORS
                                            DE 2 (bases 1 to 153586)

Birren, B., Linton, L., Musbaum, C., Lander, E., Allen, N., Anderson, M.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Madonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3122
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                                                                                                                                                                                                                                                                                                                                               Mammalia; Butheria; Pr
1 (bases 1 to 153586)
Birren,B.; Linton,L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC016316.3 GI:10045694
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens clone RP11-28K18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with Patent: WO 0200928-A 1946 03-UAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct
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Sequence 1946 from Patent WO0200928,
AX346875
                                                                                                                                                                                                                                                                                                                            Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-28K18
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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/mol type="genomic DNA"
/db_xref="texon:32630"
/note="chemically treated g
a 45 c 1537 g 4046 t
                                Ye, W.J., Zimmer, A.
(24-NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                    Metazoa; Chordata;
Sutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:18494761
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Pred. No. 4.7e+02;
); Mismatches 5;
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1-28K18, WORKING
Whitehead
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                                    and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert sizē: 152000; agarose-fp
Insert size: 152786; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.960731
Consensus quality: 149540 bases at least Q40
Consensus quality: 151261 bases at least Q30
Consensus quality: 151990 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of re
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/note="assembly_fragment"
                                                                                                       18760.
                                                                                                                                                38012.
                                                                                                                                                                                    /note="assembly_fragment"
5175. .37911
                                                                                                                                                                                                                                                                  clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"

mol_type="genomic DNA"
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                                  note="assembly_fragment"
                                                                           note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:9606"
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                                                            .93247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of 100 bp
contig of 2305
gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of 100 bp
contig of 9709 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of 100 bp
contid of 25217 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of 100 bp
contig of 31737 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of 100 bp
contig of 21331 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 5750 bp in length
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g of 10648 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23057 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKarnan, K., Meldrim, J., Meneus, L., Mihova, T., Mlanga, V., Muzphy, T., Naylor, J., Ngyen, C., Nicol, R., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Direct Submission
                                                                                                                              3 (bases I to 155229)
3 (bases I to 155229)
3 (bases I to 155229)
4 Anderson, S., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastlen, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastlen, J., Chang, J., Choepe Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Edia, J.S., Dodge, S., Dooley, K., Dorris, L., Brickson, J., Faro, Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B., Hall, J., Hotton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Marchier, K., Kamat, A., Karatas, A., Kells, C., Landers, T., Landers, Landers, Landers, Landers,
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Lindblad-Toh,K., Liu,G., Lui,A., Mau Macdonald,P., Major,J., Manning,J., Meldrim,J., Meneus,L., Mihova,T., M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-APR-2002) Whitehead Institute/MIT Center
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1 (Dases 1 to 155229)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-357G23
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Mus musculus clone RP24-357G23,
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143878. .153586
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Pred. No. 2.1e+02;
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                                                                                                               Mabbitt, R., MacLean, C.
               Matthews,C., McCarthy,M.,
Mlenga,V., Murphy,T., Naylor,J.,
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,V., Choepel,Y.,
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                                                                                                                                                                                                                                                                                                                                                             Faro, S.,
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4 ordered
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COMMENT
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 30191: contig of 30191 bp in length 30192 gap of 100 bp 30292 64548: contig of 34257 bp in length 64549 64648: gap of 100 bp 64549 124983: contig of 60335 bp in length 124984 125083: gap of 100 bp 124984 125083: gap of 100 bp 125084 155229: contig of 30146 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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Center clone name: 357_G_23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
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                                                          clone_end:T7
vector_side::
                                                                                                                                                                                                                                                                                                         vector_side:left"
                                                                                                                                                                                                                                                                                                                                                     clone_end:SP6
                                                                                                                                                         125084. .1552:
                                                                                                                                                                                 /note="assembly_fragment"
                                                                                                                                                                                                                          64649.
                                                                                                                                                                                                                                           /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:10090"
/clone="RP24-357G23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone
                                                                                                                    note="assembly_fragment
                       octor side:right"
30207 c 29719 g 45307 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type="genomic DNA"
                                                                                                                                                                                                                          .124983
                                                                                                                                                                                                                                                                                           . 64548
                                                                                                                                                                                                                                                                                                                                                                                                                                                        lib="RPCI-24 Male Mouse BAC"
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                              300 others
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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AC132362
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AUTHORS
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                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
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Best Local :
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkway, --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.9903.9 Consensus quality: 164699 bases at least Q40 Consensus quality: 164713 bases at least Q30 Consensus quality: 164718 bases at least Q20 Insert size: 165010; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Project Information ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JUN-2003) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA On Jun 10, 2003 this sequence version replaced gi:22657849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson, R.K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkway, St. Louis, MO 3 (bases 1 to 165217)
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Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases I to 165217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus chromosome UNK clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC132362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: M_BA0455B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry:
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                                                                                                                                                                                                                                                                            Quality coverage: 14.29 in Q20 bases; agarose-fp
Quality coverage: 13.37 in Q20 bases; sum-of-contigs
                                                                                       is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 165217)
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                Location/Qualifiers
                                       43960:
165217:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.2%;
83.9%;
                                   43860: contig of 43860 bp in length
43960: gap of unknown length
65217: contig of 121257 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summary Statistics
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Pred. No. 2.
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome
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4.1e+02;
5;
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                                     bp in length.
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organism="Mus musculus"

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AUTHORS
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KEYWORDS
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AC104741/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
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Best Local S
Matches 26
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  Overlapping Sequences: 5': Mapping in pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Box 352145, Seattle, WA 98195, USA
On Mar 28, 2002 this sequence version replaced gi:17975270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (21-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masses 1 to 168433)
Xaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saemphimmachak,C., Phelps,K.A., Raymond,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome
AC104741 AC025537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Saemphimmachak, C., Phelps, K.A., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC104741.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC104741
                                                                                                 Sequencing vector: plasmid; 25% of reads
Sequencing vector: M13; 25% of reads
Sequencing vector: plasmid; L08752; 49% of reads
Chemistry: Dye-terminator ET; 26% of reads
Chemistry: Dye-primer ET; 25% of reads
Chemistry: Dye-terminator Big Dye; 48% of reads
Consensus quality: 168438 bases at least Q30
Consensus quality: 168431 bases at least Q30
Consensus quality: 168431 bases at least Q20
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                                                             Quality coverage: 12.2x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                    Center project name: chr-3
Center clone name: RP11-228H5 (bc0314)
                                                                                                                                                                                                                                                                                                                                                                                                             Drafting Center: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: University of Washington Genome Center Center Code: UWGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
Mapping in progress
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/note="assembly name:Contig7"
1 35165 c 34056 g 50086 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mol_type="genomic DNA"
db_xref="taxon:10090"
chromosome="UNK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.28;
83.98;
                                                                                                                                                                                                                                                                                                                                                                                        Project Information
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Pred. No. 2.1e+02;
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3 clone RP11-228H5,
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3': RP11-14301 (UWGC:bc0262) AC025817

Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part

of this entry's ASN.1 file.

all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

Sequence Validation:

₽ S

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

1402 1442 559 <800 853 858 3605 3585 2705 2660 436 <800 1718 1703 328 <800 165 <800 10607 10473 100 <800 1126 1110 2639 2660 4989 5190 3005 3042	858 3058 <800 788 <800 1292 1900 1292 <800 4807 1900 9186 12694 426	14846 726 <800 1315 5118 1439 1442 3401 5118 2798 2761 5066 3138 796 <800 80 3138 5195 5177 498 4489 1227 1214 3337 <800 2270 2308 748 <800 1923 1900 1627 <800 1368 1340 935 1884 2604 2660 5425 8231 138 <800 1713 3138 3645 3623 2219	2361 2361 3101 3042 10526 10473 897 931 4156 4079 708 <800 3865 3915 5463 5411 11660 11718 614 <800 1461 1442 653 <800 166 <800 1314 1340 5422 553 1662 <800 462 <800 1429 1403 2347 2361 820 760 1231 1202 3192 3138 9121 9090 13263 13297 3925 3915 3637 3623 5646 5803 4069 4047 851 858 783 783 780
* consists of 21 contige. The true order of the pieces. * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. 1 101: contig of 1101 bp in length * 1102 2376: contig of 1175 bp in length * 2477 2476: gap of unknown length * 2477 5377: contig of 2901 bp in length * 3378 5478: gap of unknown length * 5378 5478: gap of unknown length * 624 7723: gap of unknown length	Sequencing vector: Mli3, 0% Sequencing vector: plasmid; 100% Chemistry: Dye-primer EF; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 166139 bases at least Q40 Consensus quality: 170280 bases at least Q20 Consensus quality: 170280 bases at least Q20 Insert size: 185000; agarose-fp Quality coverage: 5.37 in Q20 bases; sum-of-contigs Quality coverage: 4.13 in Q20 bases; sum-of-contigs Outling Coverage: 4.13 in Q20 bases; sum-of-contigs Tibes: This is a 'working draft' sequence. It currently	VERSION ACISOR40.1 GI:22218609 VERSION SUBJECT SUBJECT AUTHORS CORGANISM Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. AUTHORS TILE JOURNAL REFERENCE AUTHORS Direct Submission Submitted (14-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA Contact: Submission University Genome Sequencing Center Center: Washington University Genome Sequencing Center Center Wosc Web site:http://genome.wustl.edu/gsc/index.shtml Contact: Submissions@watson.wustl.edu Center project name: M BB0443604	Query Match Best Local Similarity 83.9%; Pred. No. 2.1e+02; Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Qy I ATAGTGAAAACTTGTGTAATTATGAAATTTT 31

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Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,

Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X.,

Gupta, J., Ho, S.-L., Idol, J., Karlins, E., Lee-Lin, S.-Q., Legaspi, R.,

Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D.,

McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.,

Snyder, B., Stantripop, S., Thomas, J. W., Thomas, P.J., Tiongson, E.E.,

Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D.,

Zhang, L.-H. and Green, B.D.

NISC Comparative Sequencing Initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovement Circle, Gaithersburg, MD 20877, USA On Nov 14, 2000 this sequence version replaced gi:10305191.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house moüse)
Mus musculus
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181191 bp DNA linear HTG 14-NOV-2000 Mus musculus chromosome 12 clone RP23-361M18 strain C57BL6/J, WORKLING DRAFT SEQUENCE, 20 unordered pieces.
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                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 167609 bases at least Q40
Consensus quality: 171224 bases at least Q30
Consensus quality: 173188 bases at least Q20
Insert size: 170000; pagarose-fp
Insert size: 182000; pulse-field-gel
Insert size: 182001; sum-of-contigs
                                                                                                                                                                                                                                                                                                               Web site: http://www.nisc.nih.gov
Contact: nisc mouse@nhgri.nih.gov
------ project Information
Center project name: sd
Center clone name: 361M18
Quality coverage: 4.62x in Q20 bases; agarose-fp Quality coverage: 4.32x in Q20 bases; pulse-field-gel Quality coverage: 4.38x in Q20 bases; sum-of-contigs
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/strain="C57BL6/J"
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chromosome="12"
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REFERENCE

(bases 1 to 202233)

Birren,B., Fasman,K., McKernan,K., Nusbaum,C., Richardson,P., Lander,E., Allen,N., Baker,J., Baldwin,J., Barna,N., Beckerly,R.,

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REFERENCE
AUTHORS
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ACCESSION
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                                                Birren,B., Fasman,K., McKernan,K., Munro,C., Nusbaum,C.,
Richardson,P., Lander,E., Baldwin,J., Barna,N., Cantu,C., Chang,A.
Cooke,P., Daly,M.J., Depayre,E., Devon,K., Dewar,K., DuRette,B.,
Forrest,C., Gage,D., Gensheimer,S., Geraigery,K., Gilmartin,T.,
Hagos,B., Halphen,I., Harris,K., Howland,J.C., Huang,J., Hui,L.,
Jacotot,L., Linton,L., MacKenzie,J., Marquis,N., McGurmott,J.,
McGurk,A., Molla,M., Morris,W., Morrow,J., Nachman,A., Naylor,J.,
O'Connor,T., Olotu,A., Peterson,K., Roberts,D., Rollins,G.,
Sarnaik,A., Shiu,P., Shyam,R., Stilwell,J., Stone,C.,
Sarnaik,A., Shiu,P., Shyam,R., Stilwell,J., Stone,C.,
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Submitted (08-DEC-1997) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.
                               Direct Submission
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/note="assembly_fragment
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1202. .92391
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Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferreira, P., Forrest, C., Gage, D., Gardyna, S., Genshelmer, S., Geralgery, K., Gilmartin, T., Gray, D., Hagos, B., Harris, K., Horton, L., Howland, J. C., Hui, L., Jacoto, L., Linton, L., MacKenzie, J., Marquis, N., McBwan, P., McGurk, A., Meldrim, J., Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Molla, M., Morris, W., Kanganath, S., Riley, R., Roberts, D., Rollins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L., Vassiliev, H., Vo, A., Stone, C., Strickland, C., Sydney, K., Tang, L., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Ye, W.J., Zemtseva, I., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                           complement(5048. .5112)
/rpt_family="AT_rich"
complement(5173. .5213)
/rpt_family="AT_rich"
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complement(3748. .377
/rpt_family="AT_rich"
         complement(13745. .14445)
/rpt_family="ilpai6"
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complement(4318, .439
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/rpt_family="AT_rich"
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/rpt_family="MER28"
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mol_type="genomic DNA"
db_xref="taxon:9606"
chromosome="17"
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     complement (36501. .36787)
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complement /1997
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PEATURES

source

COMMENT JOURNAL

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                                                            Query Match 74.2%; Score 23; DB 9; Length 202233; Best Local Similarity 83.9%; Pred. No. 2e+02; Matches 26; Conservative 0; Mismatches 5; Indels 0.
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Search completed: December 18, 2003, 09:50:15. Job time: 1396.89 secs

=> fil reg; d que 13 FILE 'REGISTRY' ENTERED AT 09:22:13 ON 18 DEC 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2003 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 17 DEC 2003 HIGHEST RN 627482-61-5 DICTIONARY FILE UPDATES: 17 DEC 2003 HIGHEST RN 627482-61-5

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2003

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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at: http://www.cas.org/ONLINE/DBSS/registryss.html

 L_2

9 SEA FILE=REGISTRY ABB=ON AUAUAGAAGCCCAAGAAAAUCAGCUGACC|GGUCAG CUGAUUUUUCUUGGGCUUCUAUAU|AUAGUGAAAACUUGUGUAAUUAUGAAAUUUU|AAAAUU UCAUAAUUACACAAGUUUUCACUAU/SQSN

Ocomplements

L3 4 SEA FILE=REGISTRY ABB=ON L2 AND SQL<101

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L3 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN

RN 290212-93-0 REGISTRY

CN GenBank AX028511 (9CI) (CA INDEX NAME)

SQL 31

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HITS AT: 1-31

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: GENBANK

L3 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN

RN 290212-92-9 REGISTRY

CN GenBank AX028510 (9CI) (CA INDEX NAME)

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HITS AT: 1-30

RELATED SEQUENCES AVAILABLE WITH SEQLINK

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L3 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN

RN 286027-93-8 REGISTRY

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HITS AT: 1 - 31

RELATED SEQUENCES AVAILABLE WITH SEQLINK

STN Files: CA, CAPLUS

L3ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN

286027-92-7 REGISTRY

13: PN: WO0042216 SEQID: 13 unclaimed DNA (9CI) (CA INDEX NAME)

SQL

SEQ 1 atatagaage ceaagaaaaa teagetgace

HITS AT: 1-30

RELATED SEQUENCES AVAILABLE WITH SEQLINK

STN Files: CA, CAPLUS

=> fil capl; s 13

FILE 'CAPLUS' ENTERED AT 09:22:48 ON 18 DEC 2003

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FILE COVERS 1907 - 18 Dec 2003 VOL 139 ISS 25 FILE LAST UPDATED: 17 Dec 2003 (20031217/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:493707 CAPLUS

DOCUMENT NUMBER: 133:130737

TITLE: Genetic predisposition to abnormal calcification

condition such as osteoporosis

Kusk, Philip INVENTOR(S):

PATENT ASSIGNEE(S): Osteometer Biotech A/S, Den.

SOURCE: PCT Int. Appl., 70 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO.

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WO 2000042216
                     A2
                            20000720
                                          WO 2000-EP319
                                                           20000117
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                     · A3
                           20001102
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             AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW; GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
             DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
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                      A2
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                                       GB 1999-1037
PRIORITY APPLN. INFO.:
                                                        A 19990118
                                       GB 1999-12585
                                                       A 19990528
                                       WO 2000-EP319
                                                       W 20000117
     Methods of assessing an individual's predisposition to abnormal
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calcification conditions such as osteoporosis by detg. the genotype of a promoter for the bone sialoprotein gene, the matrix gla protein gene, the osteoponting gene or the osteoprotegerin gene individually or in any combination. Specific allelic variations for each promoter are described.

286027-92-7 286027-93-8

RL: PRP (Properties)

(unclaimed nucleotide sequence; genetic predisposition to abnormal calcification condition such as osteoporosis)

FILE 'HOME' ENTERED AT 09:22:55 ON 18 DEC 2003

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Result
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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compugen Ltd.
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150390		
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150384	•	21.4
150384	•	21.4
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3747	69.0	21.4
2704		•
1474	•	21.4
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898	•	21.4
455		21,4
300	•	21.4
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7737	69.7	21.6
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7737 22 7737 23 7737 24 13377 24 113377 24 113379 20 910715 20 300 20 300 20 1093 22 1474 22		, , , , , , , , , , , , , , , , , , ,

ALIGNMENTS

key variation Human; bone sialoprotein; BSP; bone mineral density; atherosclerosis; osteoporosis; promoter; ds. AAA74858 standard; DNA; 31 17-JAN-2000; 2000WO-EP00319. WO200042216-A2. Homo sapiens Human bone sialoprotein gene promoter BSP-G1869A polymorphic site. 17-JAN-2001 AAA74858; 18-JAN-1999; 28-MAY-1999; 20-JUL-2000. (OSTE-) OSTEOMETER BIOTECH AS (first entry) 99GB-0001037. 99GB-0012585. Location/Qualifiers replace(16,A) /*tag= a /note= "BSP-G1869A polymorphism" 맖

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RESULT 2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                    Bone sialoprotein promoter; BSP; human; tissue-specific promoter; targetted expression; therapeutic gene; toxic gene; gene therapy; osteotropic tumour; calcification; prostate tumour; osteosarcoma; metastatic tumour; lung; breast; colon; brain; multiple myeloma; benign prostatic hypertrophy; BPH; arteriosclerosis; osteogenesis; osteoblast; bone repair; reporter construct; chromosome 4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            density. These genes include sequences encoding the bone sialoprotein, the matrix gla protein (MGP), osteopontin (OPN) and osteoprotegerin/osteoclastogenesis inhibitory factor (OPG/OCIF). A at this position is associated with a higher peak bone mass. Along with the other polymorphic sites, this variable sequence can be used to predict at individual's predisposition to osteoporosis and atherosclerosis, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence shows the polymorphic site at position 1869 of the human bone sialoprotein (BSP) gene promoter. It was used in the methods of the invention, which involve the determination of the promoter sequence at polymorphisms in a number of genes controlling bone mineral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessing predisposition to a calcification condition status such osteoporosis and atherosclerosis, comprising determining the geno of the promoter of the bone statoprotein, matrix gla protein,
                                          Novel therapeutic agent for prevention and treatment of calcified tumors and proliferative disorders such as osteosarcoma, multiple myeloma and breast cancer, comprises bone sialoprotein promoter
                Claim 5:
                                                                                                            WPI; 2000-442489/38.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone sialoprotein (BSP) promoter (-2184-+237).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA61936 standard; DNA; 2421 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteopontin or osteoprotegerin gene
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                                                                                                                                                                                                                                                                          29-JUN-2000.
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                                                                                                                                                                                                          22-DEC-1998;
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             Fig 8A-B; 79pp; English
                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                           VIRGINIA PATENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                         Chung
                                                                                                                                                                                                          98US-0113200
                                                                                                                                                                                                                                          99WO-US30642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment and
                                                                                                                                             LWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
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CC in bone, in trophoblastic cells of the placents, and in cementum and commander to the primary or at metastatic sites. This is especially evident for commander to the primary or at metastatic sites. This is especially evident for compositive metastatic to sites. This is especially evident for compositive metastatic tumours, but includes any osteotropic compositive metastatic tumour such as, for example, lung, multiple compositive metastatic cumour such as, for example, lung, multiple composition of the invention may be used to treat osteotropic composition of the invention may be used to treat osteotropic tumours commandianate growths with calcification potential) via delivery and expression of a gene encoding a protein such as herpes simplex virus composition of a gene encoding a protein such as herpes simplex virus composition for to a cytotoxic phosphorylated form. The composition may also be used to promote bone repair via delivery and expression of a gene coding a therapeutic protein such as a growth factor, a cytokine or composition in which the gene under the control of the BSP promoter is a reporter gene. Such reporter compositions may composition in which the gene under the control of the BSP promoter is a reporter gene. Such reporter compositions may content and protein such as agrowth factor. The invention content of the supressat sequence represents a human BSP promoter content is composition of the content of the fundation. The human BSP gene is located on chromosome 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel gene therapy composition comprising a mammalian bone sialoprotein (BSP) promoter operably linked to a gene sequence encoding a toxic and/or therapeutic protein contained within a delivery vector, such as a recombinant adenovirus or a liposome. The BSP promoter directs gene expression in tissue and tumour cells with calcification potential. It is active in fully-differentiated osteoblasts
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Query Match Sequence 2421 BP; 891 A; 438 C; 425 G; 667 T; 0 100.0%; Score 31; Pred. No. DB 21; other: Length 2421;

0.094

0

Gaps

0

B Ś Best Loc Matches 1860 1 ATAGIGAAAACTIGIGIAATIATGAAATTIT 31 31. ATAGTGAAAACTTGTGTAATTATGAAATTTT 1890 Conservative 0 Mismatches 0

Tocar

Similarity

RESULT 3
ABL33972
ID ABL3 ABL33972 standard; DNA; 7771 ₽₽

26-MAR-2002 (first entry)

neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antifheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy Human immune system associated gene SEQ ID NO: 1945. gene; neurofibromatosis; rheumatoid antiarteriosclerotic; Human; immune system disease; cytosine methylation; antiasthmatic; ds. antianaemic; cytostatic; nootropic; epilepsy; bowel dis anaemia;

Homo sapiens.

WO200200928-A2

03-JAN-2002

02-JUL-2001; 2001WO-EP07537.

30-JUN-2000; 01-SEP-2000; 2000DE-1032529. 2000DE-1043826.

(EPIG-) EPIGENOMICS AG

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RESULT 4

ABL33973/c.
ID ABL339

XX ABL339

XX ABL339

XX ABL339

XX ABL339

XX Human;

XW Human;

XW Human;

XW antiax

XW antiin

XW antiin

XW antiin

XW antiin

XW Homo 8

XX Homo 8

XX Homo 8

XX WO2002

XX WO1-SEP

XX WPI; 2

XX WPI; 2

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                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7771 BP; 2788 A; 45 C; 1303 G; 3635 T; 0 other;
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for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL33973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytosine methylation
                                                                Nucleic acid comprising fractor diagnosis and treatment
                                                                                                                                                                                                             30-JUN-2000; 2000DE-1032529; 01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                               cytosine
                                                                                                                WPI; 2002-130909/17
                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                             03-JAN-2002
                                                                                                                                                                                                                                                                                                                            WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                              EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1945; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                 methylation
                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 7771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antianaemic; cytostatic;
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                                                                fragment of cher
ment of diseases
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                                                                chemically modified ases associated with
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                                                               gene, useful abnormal
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03-DEC-1997; 09-SEP-1998; 14-JUN-1999;

96US-0753233. 97US-0984246. 98US-0149674. 99US-0333177.

22-NOV-1996;

11-JUN-2001; 2001US-0878574.

US2002110548-A1.

Sullivan

'n

Kriz R,

Kumar

(GEMY) GENETICS INST INC.

Claim 1;

SEQ ID

NO 1946;

32pp +

Sequence Listing;

The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polymucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The

New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transp.

transplant

Disclosure;

SEQ ID NO 8312;

dgp;

English

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                                                                                                                                          Sequence
                                                                                                                                                                            diseases. The present sequence is a gene of the
3122 ATAATAAAAACTTATATAATTATAAAATTTT
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                                                                                        Similarity
                                   ATAGTGAAAACTTGTGTAATTATGAAATTTT
                                                                                                                                          7771 BP; 2143 A; 45 C; 1537 G;
                                                                       Conservative
                                                                                        83.9%;
                                                                                                        74.2%;
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                                                                                        Score 23;
Pred. No.
                                                                       Mismatches
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                                                                                                                                            4046 T; 0 other;
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                                                                                                        Length 7771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human GDP-mannose
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20-JUN-1997;
22-JUL-1997;
                                                                                                                                               This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                               New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-)
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic protein; vaccine; Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. burgdorferi antigenic protein
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                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 124; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY19933.
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                               Similarity
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97US-0050359.
97US-0053344.
97US-0053377.
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                       69.7%;
85.7%;
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86.2%;
                                                                                                   A; 59 C; 98 G; 246 T; 0 other;
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Pred. No. 74;
                            Score 21.6;
Pred. No. 1.
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                            1.6e+02
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RESULT 7
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AC AAX616
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                  This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
                                                                                                                                   New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
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                                                                                                               Claim 1; Page 124; 275pp; English.
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RESULT 8 맑 S Matches Query Match Best Local Similarity Sequence 615 **-**24; ATAATAAAACTTATGTAATTATCAAAT 588 ATAGTGAAAACTTGTGTAATTATGAAAT 28 654 BP; Conservative 227 69.7%; 85.7%; A; 61 C; 104 G; 0 Score 21.6; DB 20 Pred. No. 1.6e+02; Mismatches 262 T; 0 other; 20; Length Indels 654; 0 Gaps

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Conservative ç Mismatches

ATAGTGAAAACTTGTGTAATTATGAAAT 28

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AAK90942

standard; DNA;

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(first entry)

经交易交易 Human digestive system antigen genomic sequence SEQ ID NO: 4518.

Human; digestive system antigen; gene therapy; cancer: appendicitis;

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			sprung's dis iverticulum;
			ease; chr.
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RESULT 9
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Best Local S
Matches 24
                                                        04-FEB-2000;
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02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                     Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; endocrine disorder; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschaprung's disease, Chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                   wound healing; sk
anti-infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                     AAS31977
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                       18-APR-2000
19-MAY-2000
                                                                                                    31-JAN-2000;
                                                                                                                          17-JAN-2001; 2001WO-US01351.
                                                                                                                                                  02-AUG-2001
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                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       Human liver associated genomic DNA #151.
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                                              17-MAR-2000;
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2000US-0180628.

2000US-0184664.

2000US-01886350.

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2000US-019123.

2000US-0205515.

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2000US-0214886.
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                                                                                                    2000US-0179065.
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                                                                                                                                                                                                                             skin aging; organ transplantation; tissue regeneration;
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Pred. No. 1.5e+02;
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Sequences AAS31827-AAS32182 represent genomic DNA molecules, which encode the liver associated polypeptides of the invention. Liver associated polypeptides are invertible in the polypeptides and their associated polypeptides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or
                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human liver related protein is used in preventing, treating or ameliorating disorders of the liver particularly cancer of the liver -
      pathological absence of a
                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457728/49.
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                                                                                                                                                                                                                                                          1; SEQ ID No 453; 526pp; English.
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2000US-0241808.
2000US-0241809.
, rabbits, goats, horses, cats, dogs, chickens or sheep. A condition can be determined by detecting the presence or mutation in a liver associated polynucleotide. The treatable
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RESULT 10
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11-JUL-2000;
14-JUL-2000;
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19-MAY-2000;
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2000US-0225213.
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                                                                                                                 The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86932) and the polymucleotide (CDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polymucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fifty wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                            Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                     Rosen
                                                                                                Sequence 7737 BP; 2397 A; 1325 C; 1490 G;
                                                                                                                                                                                                                                                                      Disclosure; SEQ ID No 2001; 673pp; English
                                                                                                                                                                                                                                                                                                                                            WPI; 2001-565190/63.
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llarity 85.7%;
Conservative
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2000US-0251989.
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2000US-0251030.
2000US-0251988.
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2000US-0251479.
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2000US-0251868.
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                                              Score 21.6; DB 23
Pred. No. 1.5e+02;
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2000US-0234223 2000US-0234274 2000US-0234997 2000US-0234998

2000US-0235484 2000US-0235834 2000US-0235836

2000US-023935 2000US-023937 2000US-0241960 2000US-0241785 2000US-0241787 2000US-0241787 2000US-0241808 2000US-0241808 2000US-0244617 2000US-0244617 2000US-0246474 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246525 2000US-0246524 2000US-0246525

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2000US-0232081

2000US-0231244 2000US-0231413

2000US-0232398

01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 05-SEP-2000;

2000US-0229344

2000US-0229509. 2000US-0229513. 2000US-0230437. 2000US-0230438. 18-AUG-2000;

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RESULT 11
ABN90332
ID ABN90332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-229509P
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RESULT 12
RAS46476
ID AAS46
XX
AC AAS46
XX
II = DE
XX
I

18-DEC-2001 AAS46476;

(first entry

AAS46476 standard; DNA; 13377

ĦP.

. 500

Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism Tumour suppressor gene derived chemically modified sequence #198

polymorphism; SNP

Ş 휴

4 GTGAAAACTTGTGTAATTATGAAATTTT 31

ĠTĠAAACATTĠTĠTĀATTACTAAATTT

4112

4085

Matches Query Match Best Local

24;

Conservative

0

Mismatches

Similarity

69.7%; 85.7%;

Score 21.6; DB 2 Pred. No. 1.5e+02

DB 24;

Length 7737; Indels

<u>.</u>

Gaps

0

2525 T; 0 other;

Sequence

7737 BP; 2397 A; 1325 C; 1490 G;

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The invention relates to 145 novel human liver antigens (ABP40831-CC ABP40975) and to cDNAs encoding them (ABN90180), and also cc encompasses polypeptides 90% identical and polynuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human liver antigen (CC prognosing or preventing various disorders of the liver. Such conditions (c. g., cytomegalovirus, Epstein-Barr virus, cc infections (e.g., Clonorchis sinensis, Echinococcus granulosus and the mese of the patitis A virus hapatitis B virus and hepatitis C virus), parasitic infections (e.g., Clonorchis sinensis, Echinococcus granulosus and continued infections (e.g., cytomegalovirus, Epstein-Barr virus, continued instolytica), and also bacterial and fungal infections. Other disorders that may be treated include inflammatory conditions (e.g., cytomegalovirus) parasitic cirrhosis and granulomatous hepatitis), damage caused by drugs or toxins, autoimmune diseases (e.g., Milson's disease, primary biliary cirrhosis), carcinoma), portal hypertension, or gastrointestinal disorders (e.g., peptic ulcers, gastritis and peritoneal diseases). Liver antigen compounds which modulate liver antigen expression or activity. The polymeptides may be used as molecular weight markers or to compounds which modulate liver antigen expression for activity. The mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as molecular weight markers or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. Sequences Abn90182-Abn90537 represent human liver antigen constructions and sequences antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2000; 2000US-244617P.
17-NOV-2000; 2000US-249299P.
08-DEC-2000; 2000US-251856P.
08-DEC-2000; 2000US-251868P.
08-DEC-2000; 2000US-251869P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding human liver antigens, useful treatment and prevention of e.g. hepatitis and hepatic related polypeptides and antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-381944/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID No 453; 181pp; English
                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C
                                                                                                                  genomic sequences.
                                            JSPTO at sequata.uspto.gov/sequence/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
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RESULT 13
ABL33463
ID ABL33
XX
AC ABL33
XX
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                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid comprising a sequence of 18 chases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CD bisuphhite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since manbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a complete expension of a tleast 9 nuclectides and may CC form part of a set of probes for detecting the cytosine methylation state cand/or single nuclectide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinuclectides e.g. CC accers and tumours. The probes can also be used in a method for CC array for analysing cytosine methylations. The parameters for the diagnosis CC and/or therapy of existing diseases or the predisposition to specific and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters, the CC differences serving as basis for diagnosis and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the CC and disadvantageous to patients. The present sequence for the complementary sequence of the corresponding odd numbered sequence (e.g. CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence (c.g. cm partner sequence).
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2000;
06-APR-2000;
07-APR-2000;
                   ABL33463;
                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not of the printed specification, but was obtained i format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                             Sequence 13377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
                                                    ABL33463 standard; DNA; 13377
                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2001; 2001WO-EP02955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                              missing).
                                                                                                                                           1827
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                                                                                                                                       GTGAAAATTTGTATAATTTTGAATTTTT 1854
                                                                                                                                                                  GTGAAAACTTGTGTAATTATGAAATTTT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No 198; 27pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                              BP :
                                                                                                                                                                                                                                                                             3714 A;
                                                                                                                                                                                                                     69.7%;
85.7%;
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                                                                                                                                                                                                                                                                           146 C; 2702 G;
                                                                                                                                                                                                          0,
                                                                                                                                                                                                        Score 21.6; DB 22
Pred. No. 1.5e+02;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                              but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                             6815
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                                                                                                                                                                                                                                                                             other;
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RESULT 14
AAX20250/G
ID AAX20
XX AAX20
XX AAX20
XX AAX20
XX BOTTE
XX BOTTE
XX BOTTE
XX BOTTE
XX Enfect
XX SOTTE
XX OS BOTTE
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDs, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fraction diagnosis and treatment cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antifheumatic; antiathritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; ALDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                         Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
                                                                                                                       Borrelia burgdorferi polynucleotide sequence
                                                                                                                                                        04-MAY-1999
                                                                                                                                                                                         AAX20250;
                                                                                                                                                                                                                   AAX20250 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13377 BP;
                             Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1436; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; as.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                GTGAAAATTTGTATAATTTTGAATTTTT 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                      (first entry)
                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                       3714 A; 146 C;
                                                            fever; endemic relapsing fever;
is; characterisation; detection;
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85.7%;
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                                                                                                                                                                                                                    111309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment of chemically modified gene, useful ment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin
                                                                                                                                                                                                                                                                                                                                                       Score 21.6; D
Pred. No. 1.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       2702 G;
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                                                                                                                                                                                                                                                                                                                                                                         .5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                       6815 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                            Lyme
ds.
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AXX20248/c
ID AXX20248 standard; DNA; 910715
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Best Local S
Matches 24
                        03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bo can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and spirochetes are pathogenic in humans and Borrelia causes epidemic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clayton R, White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 111309 BP; 35956 A; 13151 C; 19075 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-081217/07
                                                                                                                                       WO9858943-A1
                                                                                                                                                                                       Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                          Borrelia burgdorferi polynucleotide sequence
                                                                                                                                                                                                                                                                     04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
(MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1998;
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                                                                                      18-JUN-1998;
                                                                                                                                                                Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                    102865
                                                                                                                                                                                                                                                                                                                                                                                                                                     cal Similarity
24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                  ATAGTGAAAACTTGTGTAATTATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 738-800; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    ATAATAAAACTTATGTAATTATCAAAT 102838
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                   (first entry)
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97US-0050359.
97US-0053344.
97US-0053377.
                        97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                       98WO-US12764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21.6; DB 20;
Pred. No. 1.4e+02;
0; Mismatches 4;
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(HUMA-) HUMAN

GENOME SCI INC

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                                                                             Query Match
Best Local :
                                                                                                                                                                   AAX20248 to AAX20402 represent polynuclectide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and sendemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                              New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                            Sequence 910715 BP; 327171 A; 129646 C; 130753 G;
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 157-671; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-081217/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                              White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clayton R,
                                                                                                                                                         Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDIMMUNE INC
692251 ATAATAAAAACTTATGTAATTATCAAAT 692224
                                                              24;
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                                                                             Similarity
                  ATAGTGAAAACTTGTGTAATTATGAAAT 28
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dougherty
                                                                             69.7%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser
                                                           0;
                                                                               Score 21.6; DB 2
Pred. No. 1.3e+02
                                                                Mismatches
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                                                                                                                             323091 T; 54 other;
                                                                  Indels
                                                                                            Length 910715;
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                                                              Gaps
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APPLICANT: COMMERCY, 11/3

APPLICANT: COMMERCY, 11/3

APPLICANT: COMMERCY, 11/3

APPLICANT: COMMERCY, 11/3

FILE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING FITTLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE; GENEST, 051CP1

CURRENT APPLICATION NUMBER: US 09/641,638

CURRENT FILING DATE: 2000-08-16

PRIOR APPLICATION NUMBER: US 69/502,330

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: US 60/133,207

PRIOR APPLICATION NUMBER: US 60/133,207

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-05-02

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304
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                            US-09-641-638-465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 465, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pa
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-44-50 : polymorphic base T or C
NAME/KEY: misc binding
LOCATION: 502.521
OTHER INFORMATION: 12-44-50.misl, potential complement
                                            NAME/KEY: misc binding LOCATION: 489...513 OTHER INFORMATION: 12-
                                                                                         OTHER INFORMATION: upstream amplification primer, on NAME/KEY: primer bind LOCATION: 147..156 OTHER INFORMATION: downstream amplification primer
                                                                                                                                                                                     NAME/KEY: misc_binding
LOCATION: 482..500
OTHER INFORMATION: 12-44-50.mis2
                                                                                                                                                         NAME/KEY: primer_bind
LOCATION: 530..550
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                 ENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1001
                                                                                                                                                                                                                                                                                                                                                                                                                 Patent.pm
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Bougueleret, Lydie
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2451 4
4 1230025
717
                                              12-44-50 potential probe
 62.6%;
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US-07-960-981-4
PCT-US93-09634-4
US-09-064-411A-23
US-08-749-522-3
US-09-192-434-1
US-09-033-082A-23
US-09-033-082A-23
US-09-149-976-17
US-08-257-9678-10
US-08-367-841A-10
US-08-367-841A-10
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US-09-636-796A-86

US-09-636-796A-86

US-09-601-198-80

US-09-328-352-2551

4 US-09-198-452A-1
 Score 19.4;
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   벎
   4
                                                                                                                                           complement
 Length 1001;
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Sequence 86, Appl
Sequence 86, Appl
Sequence 80, Appl
Sequence 2551, App
Sequence 1778, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 17, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 10, Appl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Database

Issued_Patents_NA:*

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/cgm2_6/ptodata/2/ina/BTUS_COMB.seq:*
/cgm2_6/ptodata/2/ina/backfiles1.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1139956

569978 seqs, 220691566 residues

Title: Perfect score:

US-09-889-491-14 31

1 atagtgaaaacttgtgtaattatgaaatttt 31

Sequence: Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched:

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nucleic search,

using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.

Run on:

December 18, 2003, 09:02:17; Search time 45.2295 Seconds (without alignments) 302.521 Million cell updates/sec

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86,	86	86,	Sequence 86, Appl	86	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 134, App	Sequence 57, Appl	Sequence 294, App	•		~	00	•	•	•			216,	Sequence 117, App	ب	Sequence 1, Appli	59	Sequence 466, App	465,		Description

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                                                                                         US-09-641-638-595/c
                                                                                                             RESULT
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                                                Sequence 595, Appr
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Best Local Similarity
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CURRENT FILING DATE: 2000-08-16
CURRENT FILING DATE: 2000-08-20
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-05-07
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   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           IOCATION: 502. 521
OTHER INFORMATION: 12-44-67.mis2, potential complement
NAME/KEY: primer bind
IOCATION: 547..567
OTHER INFORMATION: upstream amplification primer, comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
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LOCATION: 481.500
OTHER INFORMATION: 12-44-67.mis1, potential
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LOCATION: 501
OTHER INFORMATION: 12-44-67 : polymorphic base T
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THER INFORMATION: downstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                            AME/KEY: primer_bind
OCATION: 164..183
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                                 INFORMATION:
                                                                                                                                                                    880 ATAGTTAGAAATTATCTAAATATGAAATT 852
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Chumakov, Ilya
Bougueleret, Lydie
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                 Blumenfeld, Marta
                                                                        Application US/09641638
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Pred. No. 1.1e
0; Mismatches
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US-09-286-691-1
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                                                                                             SEQ ID NO 1
LENGTH: 1558
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                        EARLIER APPLICATION NUMBER: PCT US97/18008
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/286,691
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,883
EARLIER FILING DATE: 1996-10-04
                                                                                                                                                                                                                                                                                                                                                     ENERAL INFORMATION:
APPLICANT: Li, xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
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PRIOR FILING DATE: 1999-02-12
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CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Amick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
                                                                                                                                                          SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Cellulases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_binding
LOCATION: 438..457
LOCATION: 438..457
LOCATION: 618..638
                  FEATURE: CDS
LOCATION: (105)..(1481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: upstream amplification primer, complement NAME/KEY: primer bind LOCATION: 235...254 CONTINE INFORMATION: downstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 12-44-181 : deletion
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LOCATION: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                           ORGANISM: Orpinomyces sp. PC-2
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les 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                951 ATAGTTAGAAATTATCTAAATATGAAATT 923
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                   and Coding
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                                                                                                                                                                                                                                                                                                                                   Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Query Match

62.6%;

Score 19.4;

DB 3;

Length 1558;

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/687,147
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/027,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-687-147.-1
                                                           PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR APPLICATION NUMBER: US 60/143,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/539,333D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Orpinomyces sp. PC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCATION: (105)..(1481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION:
                                                                                                                                                                                                        PHICANT: Essioux, Laurent
ITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
ILE REPERENCE: GENSET.047AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11, 135
40. 6268198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491
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                                CATION NUMBER: US 60/145,915
                                                                                                                                                                                                                                                                                                       Blumenfeld, Maz
Chumakov, Ilya
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Chen, Huizhong
                                                                                                                                                                                                                                                                       Bihain, Bernard
                                                                                                                                                                                                                                                                                          Bougueleret,
                                                                                                                                                                                                                                                                                                                                                                                           Application US/09539333D
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NUMBER: US 60/146,453
              1999-07-27
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79.3%;
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                                                                                                                                                                                                                                                                                                                         Marta
                                                                                                                                                                                                                                                                                          Lydie
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Pred. No. 1.1e+02;
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SEQ ID NO 117
                                                                      Matches
                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/416,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc binding LOCATION: 1502..1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 1501
OTHER INFORMATION: 99-15065-85 : polymorphic base C or G
                                                                                                                                                          LOCATION: 1489..1513
OTHER INFORMATION: 99-15065-85
                                                                                                                                                                               NAME/KEY: misc binding LOCATION: 1489..1513
                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
LOCATION: 1568..1585
OTHER INFORMATION: upstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1481..1500
OTHER INFORMATION: 99-15065-85.mis2
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                                                                                                                                                                                                                                      THER INFORMATION: downstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/146,452 FILING DATE: 1999-07-29
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 2059
                                                                      23;
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 AGTGAATAGTGGTATAAATATGAAAGTTT 2031
                                      AGTGAAAACTTGTGTAATTATGAAATTTT 31
                                                                      Conservative
                                                                                     62.6%;
79.3%;
                                                                                         Score 19.4; DB 4; Pred. No. 1.1e+02;
                                                                                                                                                             probe
                                                                        Mismatches
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                                                                                                          Length 3001;
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                                                                        Gaps
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US-09-539-333D-216/c APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKE
FILE REFERENCE: GENESET.047AUS
CURRENT PELICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR PILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30 PRIOR APPLICATION NUMBER: US 60/131,971 PRIOR FILING DATE: 1999-04-30 atent No. APPLICATION NUMBER: US 60/132,065 FILING DATE: 1999-04-30 APPLICATION NUMBER: US 60/143,928 FILING DATE: 1999-07-14 APPLICATION NUMBER: US 60/146,453 216, CATION NUMBER: US 60/145,915 Chumakov, Ilya Blumenfeld, Bihain, Bermaro **Bougueleret,** Application US/09539333D Daniel Marta Lydie

FILING DATE: 1999-07-29

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US-09-345-882-1
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SEQ ID NO 216
LENGTH: 3001
                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09345882 Patent No. 6399373 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
                                                                                                                                                                                                                                                                               APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
FILE REFERENCE: GENSET.031A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/416,384
PRIOR FILING DATE: 1999-10-12
                                                                                                                                                                                                             PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-27297-280
                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
 OTHER INFORMATION: 5-124-273
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OTHER INFORMATION: 99-27297-280.misl
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OTHER INFORMATION: 99-27297-280 :
                  NAME/KEY: allele
LOCATION: 72794
                                                    FEATURE:
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OCATION: 1761..1779
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                                                                                                      ENGTH: 162450
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                                                                                                                       NO 1
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APPLICATION NUMBER: US 60/162,288
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23; Conserv
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Pred. No. 1
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polymorphic
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                                                                                                                                                                                                                                                                                                A RETINOBLASTOMA BINDING PROTEIN (RBP-7) ASSOCIATED WITH SAID NUCLEIC ACID.
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base
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FEATURE:
NAME/KEY: allele
NAME/TON: 93714
           NAME/KBY: allele
LOCATION: 99098
OTHER INFORMATION:
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LOCATION: 90842
OTHER INFORMATION:
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                                                                                                                     NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION:
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LOCATION: 108149
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 97152
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OTHER INFORMATION:
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                                           NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION:
                                                                                 LOCATION: 134374
OTHER INFORMATION:
                                                                                                                                                           NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 106940
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LOCATION: 99117
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OTHER INFORMATION:
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LOCATION: 108106
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OTHER INFORMATION:
FEATURE:
     OCATION: 146345
THER INFORMATION:
                                                                                           NAME/KEY: allele
LOCATION: 134374
                                                                                                               FEATURE:
                                                                                                                                                    EATURE:
                                                                                                                                                                                                          AME/KEY: allele
OCATION: 108471
                                                                                                                                                                                                                                                         WAME/KBY: allele
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OCATION: 103806
                                                                                                                                                                                                                                                                                                                                               BATURE
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        5-143-101
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NAME/KEY: allele
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LOCATION: 150329
OTHER INFORMATION:
             NAME/KEY: allele
LOCATION: 99094..99140
                                                                      NAME/KEY: allele
LOCATION: 99094.,99140
                                                                                                                                                                                                                                                                                                                                              NAME/KBY: allele
LOCATION: 97099..97145
OTHER_INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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LOCATION: 160031
 THER INFORMATION:
                                                        OCATION: 99094..9
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)THER INFORMATION: polymorphic
                                                                                                                                                                                      AME/KEY: allele
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LOCATION: 97130..97177
DTHER INFORMATION: polymorphic fragment
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LOCATION: 97099..97
OTHER INFORMATION:
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OCATION: 99075..99121
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OCATION: 93690.
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OCATION: 90819..90865
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OCATION: 72771..72817
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THER INFORMATION: polymorphic
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CATION: 88050..88096
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polymorphic fragment 5-130-276 SEQ ID56
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application Patent No. 5965427
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600
                                                                                                                                                            COUNTRY: USA
ZIP: 94306
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
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TOCATION: 108127..108177
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
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LOCATION: 108127..108177
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LOCATION: 108084.
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LOCATION: 106918
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COCATION: 106918..106966
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                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNIMBER: US 08/592,126
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                        STREET: 357
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                                                                                   APPLICATION NUMBER: US OF PILING DATE: 26-JAN-1996
                                                                                                                                                      FILING DATE:
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N: polymorphic fragment 5-133-375 SEQ
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!: polymorphic fragment 5-131-395 SEQ
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                                                                                                                                                                   US/08/687,080
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PCT-US96-07709-18
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    Matches
                               Query Match
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                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: PC
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STREET:
CITY: Denver
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"S.A.
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                                                                                                          FEATURE;
                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                           NAME/KEY:
LOCATION:
                  Local
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les 22; Conservative
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                                                                                                                                                 STRANDEDNESS:
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                  Similarity
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                                                                                                                                                                                                                                        (303) 863-9700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%;
               60.6%;
76.7%;
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   0; Mismatches
               Score 18.8;
Pred. No. 1
                                                                                                                                                                                                                                                                     2618-30-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 2;
Pred. No. 1.4e+02
; DB 5;
1.9e+02;
hes 7;
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                            Length 594;
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Gaps
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RESULT 12 PCT-US96-07709-27

0

Sequence 27, Application PC/TUS9607709 GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia A. APPLICANT: Wisnewski, Nancy

CITY: Denver STATE: Colorado COUNTRY: U.S.A. ZIP: 80203

MEDIUM TYPE: Floppy disk

READABLE FORM:

TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

PARASITIC HELMINTH VENOM ANTIGEN 5-LIKE GENES AND

ALLERGEN
PROTEINS

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PCT-US96-07709-20
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                                                                 Query Match
--- Local Similarity
Conserv
                                                                Best Local Sir
Matches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application:
                                                                                                                                                                                                                                                         TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
STREET:
CITY: Denver
COlorado
"".S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 23-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tripp, Cyni
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION: PARASITIC HELMINTH VENOMITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                      ENGTH:
583 AAAGTGACATCTTCTGTTATTATCAAATAT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AAAGTGACATCTTCTGTTATTATCAAATAT 41
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                               ATAGTGAAAACTTGTGTAATTATGAAATTT 30
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                                                                                                                                                                                                                      594 base pairs
                                                                 Conservative
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                                                                                                                                                                                     single
                                                                              60.6%;
76.7%;
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                                                              Score 18.8; DB 5;
Pred. No. 1.9e+02;
0; Mismatches 7
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PROTEINS
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PCT-US96-07709-28/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ANAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                               TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFTWARE: PATENTIN Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT
                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 267
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 13
                                           SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tripp, Cyr
APPLICANT: Wisnewski,
                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 60.6%;
Local Similarity 76.7%;
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                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Denver
                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
              TOPOLOGY:
                                                                                                                                                                                                                                                      FILING DATE:
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1700 Lincoln St., Suite 3500
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                                                                                                                 (303)
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SYSTEM: PC-DOS/MS-DOS
              linear
                                                                                                                               (303) 863-9700
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) 863-0223
-- NO: 27:
                            single
                                                                                                               863-0223
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                                                                                               28:
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Pred. No. 1.9e+02;
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RESULT 15 PCT-US96-07709-26/c

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Sequence 26, Application PC/TUS9607709 GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS

NUMBER OF SEQUENCES:

Sheridan Ross & McIntosh

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Best Local &
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                                                             Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                             TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION UNMER: 32,020
REFERENCE/DOCKET NUMBER: 26:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tripp, Cyn
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                             LENGTH: 905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                  LOCATION:
                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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12 AAAGTGACATCTTCTGTTATTATCAAATAT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATAGTGAAAACTTGTGTAATTATGAAATTT 30
                              1 ATAGTGAAAACTTGTGTAATTATGAAATTT 30
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                                                                   Conservative
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                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.6%;
                                                                                                                                                                                                                                                                                                                                   863-9700
                                                                                  60.6%;
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Pred. No. 1.9e+02;
0; Mismatches 7;
                                                                                  Score 18.8; DB 5;
Pred. No. 1.8e+02;
                                                                    Mismatches
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                                                                                                 Length 905;
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                                                                      Indels
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CITY: Denver
CITY: Denver
CITY: Denver
CITY: Colorado
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: JEMM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
CLASSIFICATION:
APPLICATION NUMBER: 32,020
REGISTRATION NUMBER: 2618-30-PCT
REGISTRATION NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 905 base pairs
TEMPS mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US96-07709-26

60.6%; Score 18.8; DB 5;
Search completed: December 18, 2003, 09:04:20 Job time : 50.2295 secs
                                                                                                                                                                                             Query Match 60.6%; Score 18.8; DB 5; Length 905; Best Local Similarity 76.7%; Pred. No. 1.8e+02; Matches 23; Conservative 0; Mismatches 7; Indels
                                                                                                   894 AAAGTGACATCTTCTGTTATTATCAAATAT 865
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                            Result
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            0 0 0
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                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                    d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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31
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103.495 Million cell updates/sec
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          69.00
69.77
69.00
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m2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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m2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
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m2_6/ptodata/2/pubpna/USO9B_PUBCOMB.seq:*
m2_6/ptodata/2/pubpna/USO9B_PUBCOMB.seq:*
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9 US-09-764-887-453
10 US-09-764-887-2001
15 US-10-092-454-2001
15 US-10-093-961-453
3 US-10-311-455-1436
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3 US-10-027-632-213232
4 US-10-027-632-213232
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Sequence 8312, Ap
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PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILLING DATE: 2001-07-02
PRIOR PPLICATION NUMBER: DE 10032529.7
PRIOR FILLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILLING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1445
LENGTH: 7771
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                                                                                                            j OTHER INFORMATION: chemically treated genomic US-10-311-455-1945
                                                                  Query Match
Best Local &
                                                       Matches
                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                  Local Similarity
4650 ATAGTGAAATTTGTATAATTATGAAATTTT 4680
                                                       29;
                 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
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RESULT 2

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US-09-764-887-453
Sequence 453, Application US/09764887
Fatent No. US20020042096A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 8312
LENGTH: 134
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SEQ ID NO 1946
LENGTH: 7771
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Publication No. US20030143606A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
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CURRENT FILING DATE: 2002-12-16
CURRENT FILING DATE: 2002-07-537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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APPLICANT: PIEP!
APPLICANT: BERL!
                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANICM: Glycine max
OTHER INFORMATION: Clone ID: 701101005H1
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Pred. No. 1e+02;
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Query Match
Best Local Similarity
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US-09-764-847-2001
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                                                                                ; ORGANISM: Homo sapiens
US-10-092-154-2001
                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-092-154-2001
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; ORGANISM: Homo sapiens
US-09-764-847-2001
                                                                                                                     NUMBER OF SEQ ID NOS: 2002-03-07

Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2001

LENGTH: 7737

TYPE. """
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NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 453
LENGTH: 7737
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LENGTH: 7737
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                              Sequence 2001, Application US/10092154 Publication No. US20030054375A1
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA113
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult
NUMBER OF SEQ ID NOS: 2003
                                                                                                                                                                                                              FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                 TYPE: DNA
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Pred. No. 4.4e+02;
                               Score 21.6;
Pred. No. 4.
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Pred. No. 4.
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                                                 DB 15;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PA113C1
CURRENT APPLICATION NUMBER: US/10/073,961
CURRENT FILING DATE: 2002-03-05
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PRIOR
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R APPLICATION N
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/234,223
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5. US20030077602A1
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NUMBER: 60/236,327
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FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/231,413
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APPLICATION NUMBER: 60/236,367
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                       FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/235,836
FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/230,438
FILING DATE: 2000-09-06
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,210
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FILING DATE: 2000-08-22
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APPLICATION NUMBER: 60/241,787
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APPLICATION 1
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         NUMBER: 60/215,135
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APPLICATION NUMBER: 60/225,266

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APPLICATION NUMBER: 60/249,213
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APPLICATION NUMBER: 60/232,080
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APPLICATION NUMBER: 60/231,243
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                                                              0,
                                                             Score 21.6; DB 1.
Pred. No. 4.4e+02
0; Mismatches
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US-10-311-455-1436
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US-10-027-632-213232
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                                                                           ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-213232
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Best Local S
Matches 24
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SEQ ID NO 1436
LENGTH: 13377
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GENERAL INFORMATION:
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Query Match
Best Local Similarity 80.0
Matches 25; Conservative
                                                                                                                                                         SEQ ID NO 213232
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TITLE OF INVENTION: Diagnosis of Diseases
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OLEK,
APPLICANT: PIEPI
APPLICANT: BERL!
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PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                        ENGTH: 653
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                           APPLICATION NUMBER: US
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24; Conserv
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Score 21.4; DB 13;
Pred. No. 3.4e+02;
0; Mismatches 6;
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Pred. No. 4.8e+02
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US-10-027-632-213232
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US-10-027-632-213232
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Best Local
                                                                                                                            SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 1371
LENGIH: 2704
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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TITLE OF INVENTION: Ident
TITLE OF INVENTION: POLY
                                                                                                                                                                                                                                                              PILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/105,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PILING DATE: 1999-09-29
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NAME/KEY: misc feature
LOCATION: (1438)...(1438)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Ruben et al.
ITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
                                                                                ORGANISM: Homo sapiens
                                                                                                            TYPE: DNA
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FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
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APPLICATION NUMBER: US 60/167,363
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US-09-795-668-1/c
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SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 3747
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APPLICANT: Huei-Mei Chen
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Publication No.
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Best Local Similarity
Matches 25; Conserv
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Patent No. US20020045577A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/071,766
CURRENT FILING DATE: 2002-02-07
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                                                                                                                                                                                                                                                                              FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: U5/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Steinthorsdottir, Valgerour APPLICANT: Gulcher, Jeffrey R. TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 153:
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OTHER INFORMATION: Incyte ID No. US20020192678A1 1330122.9
NAME/KEY: unsure
LOCATION: 3223-3355
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stefansson, Hreinn
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ORGANISM: Homo sapiens
                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(1531)
                                                                                                                                                                                      TYPE: DNA
                                                DOCATION: (1)...(1531)
DIHER INFORMATION: y=t/u or c
                                                                              NAME/KEY: misc_feature
                                                                                                    THER INFORMATION: r=g or a
                                                                                                                                                                     )RGANISM: Homo sapiens
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Pred. No. 4.4e+02;
0; Mismatches 6;
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Pred. No. 4.
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US-09-795-668-1
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Patent No. US20020094954A1
GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 1503841
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ
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OTHER INFORMATION: n=a or g
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PPLICANT: Gulcher, Jeffrey R.
ITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
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Pred. No. 9.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
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CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stefansson, Hreinn kappliCANT: Stefanthorsdottir, Valgerdur APPLICANT: Gulcher, Jeffrey R. HINGENTION: HUMAN SCHIZOPHRENIA FILE REFERENCE: 2345.2004-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: b=g
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Search completed: December 18, 2003, 10:23:13 Job time : 1014.1 secs
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; NAME/KEY: misc feature
; LOCATION: (1)....(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1
                                                                                                                                                                       Query Match 69.0%; Score 21.4; DB 10; Best Local Similarity 80.6%; Pred. No. 9.5e+02; Matches 25; Conservative 0; Mismatches 6;
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Aedes aegypti
Endaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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RESULT 3
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Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aed
1 (bases 1 to 242)
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CSU-K33r.34G16.SP6 CSU-K33r Aedes aegypti
CSU-K33r.34G16, genomic survey sequence.
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Library was provided by Susan
State University.
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Contact: Brendan Loftus
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End sequencing of Aedes aegypti BACs
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/db_xref="taxon:7159"
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/clone_lib="CSU-K33r.34616"
/clone_lib="CSU-K33r"
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/mol type="genomic DNA"
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Eukaryota, Endopterygota, Diptera,
1 (bases 1 to 537)
Loftus, B., Shetty, J., Knudson, D. a
BAC end sequencing of Aedes aegypt
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                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedt (bases 1 to 696)
Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D. End sequencing of Aedes aegypti BACs
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David
Seq primer: T7
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Department of Bukaryotic
                                                                                                                                                                                                                                                      Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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Aedes amounti
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                                Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                        Other GSSs: CSU-K33r.15020.SP6
Contact: Brendan Loftus
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Email: enta@tigr.org
Library was provided
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/clone="MDL.35011"
/clone="MDL.35011"
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Hongbin Zhang"
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mol_type="genomic DNA"
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Aedes aegypti
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Pred. No. 2.1e+02;
 Susan Brown
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   and Dennis Knudson at Colorado
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574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                            Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC116481.1 GI:29985536
                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other GSSs: NDL.60K24.SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera, Endopterygota, Diptera, Nematocera, Cu
1 (Dases 1-to 850)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neontera; Endopteryqota; Diptera; Nematocera; Culicoidea; Aed
                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan Loftus
                                                                           Similarity
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/clone="CSU-K33r.15020"
/clone_lib="CSU-K33r"
/note="Vector: pBeloBBC11; S
a 173 c 121 g 203 t
                                                                                                                                    /clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site 1: Hind III, The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
106 c 201 g 281 t
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mol_type="genomic DNA"

/strain="Rexville"
                                                                                                                                                                                                                                                               /organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
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Tetraodon nigroviridis genome survey sequence T7 end of clone
205A06 of library G from Tetraodon nigroviridis, genomic survey
AQ515182
HS 2208 B2 E05 T
sapiens genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/fetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferish Tetracoon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          using rect. 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                     /note="Genoscope sequence ID : COAG205BA03LP1~end : 154 c 0 g 172 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                 'clone="205A06"
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      543 bp DNA linear GSS 05-MA:
T7C CIT Approved Human Genomic Sperm Library D
C clone Plate=2208 Col=10 Row=J, genomic survey
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Fax: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2208 row: J column: 10
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 543.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood I
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 543)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., 1 (bases) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. ar
                   Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                     AZ997354.1 GI:13868581
AZ997354.1 GI:13868581
GSS.
                                                                                                                                                                                                                                                                                                                                                         AZ997354 595 bp DNA linear GSS 27-APR-200200283B21R Mouse 10kb plasmid UUGCZM library Mus musculus genomic clone UUGCZM0283B21 R, genomic survey sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 595)
                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                        Mus
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                            plasmid inserts
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                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ass: BAC ends
                                                                                                                                                                                                                                                                                    musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CIT Approved Human Genomic Sperm
/note="Organ: sperm; Vector: pBeloBAC11; BAC
B-Coli DH10B"
1 108 c 99 a
     Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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                                         Genome Center
                                                           Weiss
 Polymers Research
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Pred. No.
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7.5e+02;
Bldg.,
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 2030 B.,
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                                                                                                                                                                                                                              Murinae; Mus
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ORGANISM
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VERSION
KEYWORDS
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AZ868713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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High quality sequence stop: 595.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0.83 row: B column: 21
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 616)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                             2M0180I02R Mouse 10kb plasmid
clone UUGC2M0180I02 R, genomic
University of Utah
University of Utah
                                             Contact: Robert B.
                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                      AZ868713.1 GI:13072302
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                                                                 Unpublished
                                                                                         plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTTGAAAACTTGTGTCATTCTAAAATTTT 392
                                                                                                                                                                                                                                                                                                                    musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. coli strain XLI0-Gold, T1-resist/Colone lib="Mouse 10%b plasmid UUGC2M library/note="Vector: pWp42nv, Purified genomic DNA: musculus C57BL/6J (female) was obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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'mol_type="qenomic מאז"
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strain="CS7BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:10090"
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                        Genome Center
                                             Weiss
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence
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smid UUGCIM library Mus musculus genomic
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7.6e+02;
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                                                                                                                                                                                                                                                     Murinae; Mus.
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REFERENCE
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Best Local
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Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: I column: 02
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Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soafes, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 616.
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 668)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE:5844434 3', mRNA sequence.
BQ002494
BQ002494.1 GI:19727394
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                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                           Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mol_type="genomic DNA"
/strain="C57BL/6J"
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83.9%;
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Pred. No.
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7.7e+02;
5;
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CDNA clone
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; Homo.
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B

FEATURES

Library was provided by David Severson Seq primer: T7

Class: BAC ends.

Tel: 301-838-3543 Fax: 301-838-0208

Email: enta@tigr.org

9712 Medical Center Drive, Rockville,

MD 20850,

source

organism="Aedes aegypti"/ Location/Qualifiers Ś

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REFERENCE
AUTHORS
TITLE
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ORGANISM
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VERSION
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CC120192/c
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                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be through the I.M.A.G.B. Consortium/LLNL at: http://image.lln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
                                                                                                                                                                                                                                                                                                 CC120192 814 bp DNA NDL.51F5.T7 Notre Dame Liverpool Aedes NDL.51F5, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 FORWARD
                                                             Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes. 1 (bases 1 to 814)
Lofetus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
                                                                                                                                                           Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                        Contact: Brendan Loftus
                                                                                                                                                                                                                                                       CC120192
CC120192.1 GI:29989247
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Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone libe NGI GAP EII"
//clone libe NGI GAP EII"
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
consetructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_SEQ=ACACTTGCAC"
96 c 114 g
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TAG_TISSUE=chondrosarcoma
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of Eukaryotic Genomics
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83.98;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 bp sam04f09.y1 Gm-c1063 Glycine max Gm-c1063-4506 5', mENA sequence BM885747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
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                                                                                                                                                                                                                                                                                            Putative full length read vector to vector length is 233 Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available through: ResGen, Invitrogen Cory South Memorial Parkway Huntsville, AL 35801 For further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoemaker, R., Keim, P., Vockin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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EST.
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BM885747
                                                                                                                                                                                                                                                                                                                                                                                                          call: (800)-533-4363 or contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,Y., Person,B., Swaller,T., Gibbons,M., Pape,I
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y.,
,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hongbin
a 210
               /clone lib="Gm-c1063"
/notes"Vector: pBluescript II SK+; Site 1: BcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from germinating shoots of the cultivar Williams. The
seeds were allowed to germinate for 24 hours prior to
harvesting the germinating shoots. Complementary DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvad
by David Severson at the University of Notre Dame and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Liverpool"
/db_xref="taxon;7159"
/clone="NDL.51F5"
synthesized from mRNA using
                                                                                                                                                                                       /db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:
                                                                                                                                                                                                                                                        organism="Glycine max"
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                                                                                                                                                   tissue_type="Germinating
lab_host="DH10B"
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cDNA clone SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                          ccu@resgen.com web site:
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                                                                                                                                                                     Gm-c1063-4506"
shoot, 24 hour
a primer consisting
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Glycine max
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 618 Std Error: 0.00
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Public Soybean BST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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/clone lib="Gm-c1040"
/clone lib="Gm-c1040"
/clone lib="Gm-c1040"
/note="Vector: pT7T3Pac (Pharmacia); Site 1: EcoRI;
Site 2: NotI; This cDNA library was constructed from mRNA
sice 2: NotI; This cDNA library was constructed from mRNA
isolated from hypocoty1 and plumule tissues of seeds
germinated for three days of the cultivar Williams 82.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
site. EcoRI adapters were ligated to the blunt-ended cDNA
in the construction of the difference of the construction of the constr
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clone="GENOME SYSTEMS CLONE ID: Gm-c1040-2149"
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lab_host="DH10B"
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Gm-c1087-5369 5' similar to TR:Q43015 Q43015 ALCOHOL
DEHYDROGENASE-1CN ; mRNA serveror
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., A., Bolla, B., Marra, M., Biller, T., Theising, B., Allen, M., Bowers Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R., and Wilson, R.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Public Soybean EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis,
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BQ611630.1 GI:21601299
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Location/Qualifiers
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Putative full length read
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                                                          /note=Wector: pBluescript II SK+, Site_1: EcoRI; Site_2: KhoI; The mRNA was prepared using polyatract mRNA system from PROMESA. The CONA was prepared using the STRATAGENER kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI primer consisting of a poly(dT) sequence with a XhoI
                                                                                                                                                                                                                                                /mol_type="manA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; rosid;
; eurosids II; Brassicales; Brassicaceae; Brassicacea;
[ (bases 1 to 565)
1 (bases 1 to 565)
1 (Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
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25; Conser
                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole genome shotgun sequencing of Brassica oleracea Unpublished Other_GSSs: BOMSU91TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS
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                                                                                                                                                                                                                                                                                                                                  Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                 DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                   Smail: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chris Town
                                                                                Similarity
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nilarity 86.2%;
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38 c 127 g 162 t
                                                                                                                                            /clone lib="BO 2 3 KB"
/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
a 110 c 80 g 201 t
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1. .565
                                                                                                                                                                                                                                  /organism="Brassica oleracea"
(mol_type="genomic DNA"
(strain="mol000DH3"
db_xref="taxon:3712"
                                                                                                                                                                                                                   clone="BOMSU91"
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Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oleracea
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                                                                                1e+03;
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Protein disulphide

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Maximum Match 100%
Listing first 45 summaries
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AAA74857
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ABA05477
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               Human bone sialopr
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           Human RNA gyrase 1
#2407 used t
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                                                                                                                                                                                                  Human; bone sialoprotein; BSP; bone mineral density; atherosclerosis; osteoporosis; promoter; ds.
                                                                                                                                           AAA74857;
                                                                          variation
                                                                                                                     Human bone sialoprotein gene promoter BSP-A1496G polymorphic site.
                                                                                                                                17-JAN-2001
                                                                                                                                                      AAA74857 standard; DNA; 30
                 18-JAN-1999;
28-MAY-1999;
                                17-JAN-2000; 2000WO-EP00319.
                                           20-JUL-2000.
                                                     WO200042216-A2.
                                                                                           Homo sapiens.
     (OSTE-) OSTEOMETER BIOTECH AS
                                                                                                                                                                                                                                                 (first entry)
                 99GB-0001037.
99GB-0012585.
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/*tage a
/*note= "BSP-A1496G polymorphism"
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AAI38122
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Result No.

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RESULT 2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kusk
                                                                                   Novel therapeutic agent for prevention and treatment of calcified tumors and proliferative disorders such as osteosarcoma, multiple myeloma and breast cancer, comprises bone sialoprotein promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bone sialoprotein promoter; BSP; human; tissue-specific promoter; targetted expression; therapeutic gene; toxic gene; gene therapy; osteotropic tumour; calcification; prostate tumour; osteosarcoma; metastatic tumour; lung; breast; colon; brain; multiple myeloma; benign prostatic hypertrophy; BPH; arteriosclerosis; osteogenesis; osteoblast; bone repair; reporter construct; chromosome 4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30 BP; 14 A; 7 C; 5 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-476070/41.
                         Claim 5; Fig 8A-B; 79pp; English.
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                                                                                                                                                                                                              WPI; 2000-442489/38
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CC in hone, in trophoblastic cells of the placents, and in cementum and CC dentin of teeth. It is also active in a variety of human tumours or commendation of teeth. It is also active in a variety of human tumours or commendation of teeth. It is also active in a variety of human tumours or commendation or at metastatic sites. This is especially evident for prostate and osteosarcoma tumours, but includes any osteotropic composition and brain. The BSP promoter may also be expressed in non-malignant conditions in which calcification occurs, such as benign composition of the invention may be used to tradt osteotropic tumours composition of the invention may be used to tradt osteotropic tumours composition of a gene encoding a protein such as herpes simplex virus thymidiane kinase (HSVYK), which converts prodrugs such as acyclovir and composition of a gene repair via delivery and expression of a gene canoding a therapeutic protein such as a growth factor, a cyclovir and colony stimulating factor, or an angiogenic factor. The invention calso discloses a composition in which the gene under the control of the BSP promoter is a reporter gene. Such reporter obspections may be used to identify composition in which the gene under the control of the BSP promoter is a reporter gene. Such reporter a human BSP promoter control of the BSP promoter is a claimed for use in the compositions of the invention. The human BSP gene is located on chromosome 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel gene therapy composition comprising a mammalian bone statoprotein (BSP) promoter operably linked to a gene sequence encoding a toxic and/or transpecture protein contained within a delivery vector, such as a recombinant adenovirus or a liposome. The BSP promoter directs gene expression in tissue and tumour cells with calcification potential. It is active in fully differentiated osteoblasts
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Sequence 2421 BP; 891 A; 438 C; 425 Ģ 667 T; 0 other; Length 2421;

Query Match Best Local S Matches 30 l Similarity 30; Conserv 100.0%; ilarity 100.0%; Conservative 0; 0; Score Pred. Mismatches 30; ő 0.015; 0 <u>.</u> Gaps 0

DB 21;

片 1487 ATATAGAAGCCCAAGAAAAATCAGCTGACC 1516

8

ATATAGAAGCCCAAGAAAAATCAGCTGACC 30

RESULT 3

AAS53160 standard; DNA;

13-FEB-2002 (first entry)

Enterococcus faecalis DNA for cellular proliferation protein #588.

Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.

Enterococcus faecalis.

WO200170955-A2

27-SEP-2001

21-MAR-2001; 2001WO-US09180.

26-MAY-2000; 23-OCT-2000; 27-NOV-2000; 21-MAR-2000; 23-MAY-2000; 2000US-206848P. 2000US-207727P. 2000US-242578P.

2000US-191078P.

2000US-257931P 2001US-269308P 2000US-253625P.

(ELIT-) ELITRA PHARM INC

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RESULT 4
AAX12984/c
ID AAX129
XX AAX129
XX AAX129
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XX Ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the Genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence is also useful to screen CC wide variety of organisms. The present sequence encodes an CC a wide variety of organisms. The present sequence encodes an CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIPO at CC format directly from WIPO at
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06-MAY-1997;
16-MAY-1997;
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Yamamoto RT,
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                            WPI; 1999-045171/04
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                                                                                 Dillon PJ,
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Xu HH;
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                                                                                                                                    GENOME SCI INC
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97US-0044031.
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Pred. No. 21;
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New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
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Claim 1; Page 429-438; 2084pp; English.

primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences A computer readable medium has been developed which has recorded on 982 nucleotide sequences isolated from the Enterococcus faecalis ger AAX12938 to AAX13919 represent these nucleotide sequences which are be used in vaccines to prevent or attenuate an Enterococcal on it genome

Sequence 17087 BP; 4734 A; 3683 ü 3245 9 5415 1-3 10 other;

Query Match Matches Best Local 24; Similarity Conservative 88.9%; 74.0%; 0; Score 22.2; Pred. No. 26; Mismatches B 20; ω Length 17087; 0 Gaps

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띩 S 11327 4 ТАСААСССКАВААААТСАССТВАСС 30 TAGAAGCCGAAGAAAAATCAGTTGAAC 11301

ABS98779 standard; DNA; 17087 Β₽

ABS98779

18-DEC-2002 (first entry)

Enterococcus faecalis contig sequence #47.

RESULT 5
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ID ABS9877
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KW pathog
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KW contig
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KW contig
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XX pathogenicity; vaccine; resistance; Enterococcal infection; commercial; therapeutic; industrial; fermenting; sugar source; metabolite; vaccine; biochip technology; antibacterial; modulator of nucleic acid expression; Computer readable medium; Enterococcus faecalis; microbe; growth;

US2002120116-A1

Enterococcus faecalis.

29-AUG-2002.

04-MAY-1998; 98US-0070927.

04-MAY-1998; 98US-0070927

(KUNS/) (BARA/)) KUNSCH C A.) DILLON P J.) BARASH S.

Kunsch CA, Dillon 'n Barash ŝ

WPI; 2002-750065/81.

Computer readable medium having two nucleotide sequence useful for determine infections in animals having recorded on it a Enterococcus faecalis ul for detecting diseases related to

Claim 1; Page -; 119pp; English

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RESULT 6
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this polypeptide and DNA recombinant techniques to produce this polypeptide. The present invention also discloses a method of applying this polypeptide to treat various diseases, such as malignant tumour,
                                                                                                                                                                                                                   New polypeptide-human RNA unwindase 12 and polynucleotide encoding polypeptide -
                                                                                                                                                                                                                                                                                                                        WPI; 2002-049927/07.
P-PSDB; AAM47948.
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from USPTO at http.sequdata.uspto.gov.
                                                                                              The invention relates to human RWA gyrase 12, the polynucleotide encoding
                                                                                                                                                       Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2000; 2000CN-0111862.
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/product= "RNA gyrase
/note= "claimed in cla
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Best Local :
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                                                                                                                             The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequen (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation st and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2528 BP; 815 A; 518 C; 568 G; 627 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2000; 2000DE-1013847; 06-APR-2000; 2000DE-1019058; 07-APR-2000; 2000DE-1019173; 30-JUN-2000; 2000DE-1032529; 01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200168912-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour suppressor gene derived chemically modified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 411; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001; 2001WO-EP02955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAMAGAMACTCAAGAMAMATCATATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological diseases and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                               sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP;
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diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events where disadvantageous to pattents, The present sequence is one of the same disadvantageous to pattents, The present sequence is one of the same disadvantageous derived from tumour suppressor genes and

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ATAGAAGCCCAAGAAAAATCAGCTGACC

Best Local Similarity

Conservative

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Pred. No. Mismatches 80

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RESULT 8
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Best Local :
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Note: The sequence data for this patent did not of the printed specification, but was obtained i format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                   The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ARM93503-ARM97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method of the invention has hepatotropic, and the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug register as the cancer that can be used to monitor disease states, disease progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a prinvolves detecting the level of expression of two or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2001; 2001WO-US30589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene #2407 used to diagnose liver cancer.
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                                                                                                drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-426119/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver tissue sample
                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; SEQ ID NO 2407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298pp; English
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Pred. No. 1.2e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T; 4
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in electronic
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Query Match

Sequence

3610

BP; 1322 A; 622 C; 963 G;

703 T; 0 other;

66.7%; Score 20;

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24;

Length 3610;

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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.
                                                                                                                                                                                                                                                                                                                                            15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                        ABL62384;
                                                                                                                                                                                                                                                                                                                                                                   ABL62384 standard; DNA; 3610 BP.
                                                                                                                                                                                                                                                       30-MAY-2001; 2001WO-US10838
                                                                                                                                                                                                                                                                              WO200194629-A2
                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                 Colon adenocarcinoma related gene sequence SEQ ID NO:721
                                                                                                        28-SEP-2000
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RESULT 10
ABLG6804
ID ABLG68
XX ABLG68
AC ABLG68
XX IS-MA
ID Kidne
XX Humar
KW Stome
KW Gytos
KW Gyene;
XX W0200
XX Homo
XX IS-DI
PR 30-M
XX PR 18-SI
PR 20-S
PR 20-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC expression of at least one gene (I) of a signature gene set, where (I) CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL/61644 CC to ABL/70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic cativity and can be used in gene therapy. M1 can be used for screening CC antivity and can be used for producing a product which CC is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC oscophageal, ovarian, kidney, prostate or panoreatic cancer, affiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and Wilm's tumour.
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Best Local S
Matches 23
                                               18-SEP-2000;
18-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young PE,
Soppet DR,
                                                                                               05-JUN-2000;
                                                                                                                                                                                              WO200194629-A2
                                                                                                                                                                                                                                                                         Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                        Kidney cancer related gene sequence SEQ ID NO:6941.
                                                                                                                                                                                                                                                                                                                                                                                                          ABL68604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3610 BP; 1322 A; 622 C; 963 G; 703 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method (M1) for screening for anti-neoplastic agent. The method involves exposing cells to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 721; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                             30-MAY-2001; 2001WO-US10838.
                                                                                                                                                               13-DEC-2001
                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL68604 standard; DNA; 3610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1112
                                                                                                                                                                                                                                                             da.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Weaver Z;
2000US-209473P.
2000US-209531P.
2000US-23313SP.
2000US-233617P.
2000US-234009P.
2000US-234009P.
2000US-234039P.
2000US-234039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
82.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 1.6e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3610;
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Matches

23;

Conservative

Query Match Best Local Similarity

66.7%;

; Score 20; DB; ; Pred. No. 1.6e. 0; Mismatches

; DB 24; I . 1.6e+02; tches 5;

Length 3610; Indels

0

Gaps

0

Sequence

3610 BP; 1322 A; 622 C; 963 G;

703 T; 0 other;

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The present invention describes a method (M1) for screening for an CC anti-neoplastic agent. The method involves exposing cells to a chemical CC agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 847 sequences (given in ABL6164 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening CC anti-neoplastic agent, and can be used for producing a product which CC is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC estructure and/or properties of the agent. M1 can be used in the CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC escophageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
03-OCT-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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Soppet DR,
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28-SEP-2000;
28-SEP-2000;
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22-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                   Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                         Claim 1; SBQ ID 6941; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-188264/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                        Augustus M, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-244867P
2000US-245084P
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                                                                                                                                                                                                                                                                                                                                                                                                                         Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                         Endress G,
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RESULT 11
RELIT 71
RACIA ASILIT
XX ABILIT
XX ABILIT
XX Dross
XX Clai
XX NPI;
XX NPI;
XX NPI;
XX NPI;
XX NPI;
XX Clai
RESULT 12
ABA90521/G
ID ABA90
XX
AC ABA90
XX
DT 16-MA
XX
DE Genom
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Best Local Similarity
                                                                                                                                                       0521/c
ABA90521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231.
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  Genomic sequence of Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5088 BP; 1622 A; 1000 C; 938 G; 1528 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3187; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting genes from Drosophila and for elucidating cell signalling
                                                 16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences (ABL0184)
(ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                       standard;
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                                                    (first entry)
                                                                                                                                                       DNA; 2365589 BP
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Pred. No. 1.7e
0; Mismatches
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1.7e+02;
5;
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and cell-cell
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AAH72236/c
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABS3300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent wo200177334 (published 18-CCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleotide sequence useful in the identification lactis and related species - {\color{black} }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000; 2000FR-0004630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 1; 2504pp; French.
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                                    21-DEC-1999;
14-MAR-2000;
                                                                                                                                                                                                                          Human cervical cancer marker
                                                                                                                                                                                                                                                    19-SEP-2001
                                                                                                                                                                                                                                                                                                        AAH72236 standard;
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                                                                                        08-DEC-2000;
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                Cervical cancer;
                                                                                                                                                                                                                                                                              AAH72236;
         12-MAY-2000;
                                                             08-DEC-1999;
                                                                                                                   14-JUN-2001.
                                                                                                                                            MO200142467-A2
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                                                                                                                                                                                                                                                    (first entry
                                                                                         2000WO-US33312.
 2000US-0220114
            2000US-0203791
2000US-0210600
                                     99US-0171350.
2000US-0189315.
                                                                9908-0169681
                                                                                                                                                                                              cytostatic;
                                                                                                                                                                                                                                                                                                        CDNA; 508
                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 24;
Pred. No. 3.1e+02;
0; Mismatches 5;
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                                                                                                                                                                                                pre-malignant condition;
                                                                                                                                                                                                                          nucleic acid 3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2365589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or Lactococcus
                                                                                                                                                                                                   gene therapy;
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RESULT 14
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The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful; to assess if a patient is afflicted with
                                                                                                                                                                                                                                                                                                                                                                                       Human cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 508 BP; 108 A; 143 C; 129 G; 128 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                 Claim 1;
                                                                                                             WPI; 2001-375006/39.
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                                                                        isolated nucleic for assessing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer -
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                                                                       assessing
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                                              Page 215-216; 1051pp; English.
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2000US-0189315.

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                                                                    acid for diagnosing and treating cervical cancer detecting compounds for treating the cancer -
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Query Match Best Local : Matches

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for gene therapy.

polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be inhibiting cervical cancer in a patient. The nucleic acids may also be

The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded

Page 513; 1051pp; English.

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer -
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Post-processing: Minimum Match 0%
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US-08-98-207A-37
US-08-98-2077-129
US-09-685-2073-17
US-09-685-853A-3
US-09-685-853A-3
US-09-685-853A-3
US-09-614-034-189

US-09-675-305-5

US-09-18-352-1822

US-09-107-522A-2701

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                          Sequence 5, Appli
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US-09-453-702B-189	US-08-998-416-289	US-08-998-416-1138	US-08-998-416-187	US-09-198-452A-1	US-09-173-914-6	US-08-961-527-61	US-08-738-349-5	US-08-738-349-3	US-08-580-031A-4	US-08-332-638-57	US-08-332-643-51	US-08-188-228-57	US-09-252-991A-1417	US-09-328-352-507	US-09-252-991A-1191	US-09-381-849-6	US-08-716-301-5
Sequence 189, App	Sequence 289, App	Sequence 1138, Ap	Sequence 187, App	Sequence 1; Appli	Sequence 6, Appli	Sequence 61, Appl	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 57, Appl	Sequence 51, Appl	Sequence 57, Appl	Sequence 1417, Ap	Sequence 507, App	Sequence 1191, Ap	Sequence 6, Appli	Sequence 5, Appli

ALIGNMENTS

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,036

PILING DATE: 06-UN-1995

CLASSIFICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US 08/184,605

FILING DATE: 21-DAM-1994

ATTORNEY/AGENT INFORMATION:
NAME: No. 5728806and, Greta E.

PECTSTRATION NUMBER: 35,302

PROST STRATION NUMBER: 27866/31784
US-08-468-036-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-468-036-4/c
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Patent No. 5728806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATENT NO. 5728806

GENERAL INFORMATION:
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Hockstra, Merl F.
                                                                                                                                                                                             TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 6854 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                      MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Materials and TITLE OF INVENTION: Interact with
                  NAME/KEY:
                                                                                                                                                                                                                    TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America ZIP: 60606-6402
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                CDS
2050..4053
                                                                         DNA (genomic)
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Casein Kinease I
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Query Match

64.78;

Score 19.4;

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Length 6854;

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                                                                                                                                                                                                                                        US-08-376-843-4
                                                                                                                                                                                Matches
                                                                                                                                                                                             Query Match
Best Local (
                                         Patent No.
                                                                     08-441-139-17
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: No. 5846764and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DeMaggio, Anthony J.

APPLICANT: Hockstra, Merl F.

TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: that Interact with Casein Kinase I
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                            ropology:
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                                                                                                                           2644 ÁTÁAÁGÁATCCAÁAGAÁAGATTÁGATGAC 2616
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30. 5846764
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                           INFORMATION:
                                                                                                                                                    1 ATATAGAAGCCCAAGAAAAATCAGCTGAC 29
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                                            5773245
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                     Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Marshall, O'Toc
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Wittrup, Dr. Karl D. Robinson, Anne S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                    2050..4053
                                                                                                                                                                                                                                                                                             DNA (genomic)
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                                                                                                                                                                                                                                                                                                                        single
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79.3%;
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lower, 233
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                                                                                                                                                                               Score 19.4; I
Pred. No. 38;
0; Mismatches
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); Mismatches
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South Wacker Drive
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

ODERATING SYSTEM: PC-DOS/MS-DOS

ODERATING SYSTEM: PC-DOS/MS-DOS

CITY: Chicago STATE: Tllino

Illinois

ZIP: 60606-6402

COUNTRY: United States of America

SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:

Version

FILING DATE:

06-JUN-1995

US/08/468,036

APPLICATION NUMBER:

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US-08-441-139-17
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                                                                                                                                                                                               RESULT 4
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Tocal Similarity
                                                                                                                                        Sequence 38, Appr. S72880/
                                                                                                                                                                                                                                                                                                             Matches
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2403 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING LALLON: 435
CLASSIFICATION: 435
ERIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: 06-001-1993
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                TITLE OF INVENTION:
                                                                                              APPLICANT: DeMaggio, Anthony J. APPLICANT: Hoekstra, Merl F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 516-742-4343
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 516-742-4366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
STREET:
                 ADDRESSEE:
                                                                                                                                                                                                                                               1929
                                                   OF SEQUENCES:
                                                                                                                                                                                                                                                                  AGAAGCCCAAGAAAATCAGCTGA 28
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA (genomic)
                                                                                                                                                                                                                                               AGAAGCCCAGGAAAAAGCTGCTGA 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X
                                                                                                                                                               Application US/08468036
3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          double
                                                                                                                                                                                                                                                                                                                          64.0%;
87.5%;
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                                                                Materials and Methods Relating to Proteins that Interact with Casein Kinease I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
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Pred. No. 39;
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                             Length 2403;
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RESULT 5
US-08-376-843-38/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                        TELEFAX: 312/474-0448
TELE: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3466 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3466 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                            APPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                           NAME: NO. 5846764and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DeMaggio,
APPLICANT: Hoekstra,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: Materials and Methods Relating to Proteins ITLE OF INVENTION: that Interact with Casein Kinase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBER OF SEQUENCES:
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REGISTRATION NUMBER: 35,302
                          LENGTH: 3466 base pairs
                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Marshall, O'Toole,
6300 Sears Tower, 233
                                                                                                           312/474-6300
312/474-0448
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linear
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                                                                           38:
                                                                                                                                                                                              Greta E.
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Pred. No. 41
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South Wacker Drive
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US-08-686-878A-8/c

Sequence 8, Application US/08686878A Patent No. 5708157

GENERAL INFORMATION:

APPLICANT:

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US-08-376-843-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
RESULT 7
                                                                                                                                            ; ORGANISM:
US-08-728-956-2
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Best Local Similarity
                                                                                        Matches
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5677175
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                 MOLECULE NO PURCE: NO
                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                  TELEPHONE: (317) 231-7745
                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
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APPLICANT: McGee, J.
                                                                                                                                                                                                                                                                                                                                                       NAME: Breen, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                              LENGTH: 613 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                     TRANDEDNESS: dov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 ÁTAGAGAAGCCGAAGGAAAATCAG 330
                                      292 TTGAAGCAGAAAAAAGCAGCTGAGC 318
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5. 5677175
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                                                                                       Conservative
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                                                                                                                                                                                                           DNA (genomic)
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                                                                                                     63.3%;
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                                                                                                     Score 19;
Pred. No.
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Pred. No. 41;
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37;
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                                                                                                                   Length 613;
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                                SOFTWARE: PatentIn Ver.
SEQ ID NO 13
LENGTH: 429
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                                                                                  APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                   APPLICANT: Mi, Sha
                                                                                                                                                                                                                                                                         APPLICANT: Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                   APPLICANT: Merberg, David
                                                                                                                                                                                                                                                         PPLICANT: Evans, Cheryl
                                                                                                                                                                                                                                                                                            PPLICANT: McCoy, John M.
PPLICANT: LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Spatialing, Vikki
APPLICANT: Spatialing, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYMUCLECTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 TACAGAAGCCCAAGAAAGAGCAAGAGAC 306
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22; Conserv
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DEDNESS: double
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429 base pairs
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Merberg, Maurice
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                                                                                                                                                                                                                                                                                                                                  Kenneth
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Pred. No. 62;
0; Mismatches
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US-08-936-165A-189
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Best Local Similarity
Matches 22; Conserv
           ZIP: 1946-039
ZIP: 1946-039
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAMB: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (142)..(143)
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LOCATION: (18)...
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LOCATION: (117)
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LOCATION: (24)
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LOCATION: (97)
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
                                                                                                                                                                                                                                                                                             STREET: 705 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 TACAGAAGCCCAAGAAAGAGCAAGAGAGAC 306
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N: No. 6348582el Prokaryotic Polynucleotides,
N: Polypeptides and Their Uses
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Michael
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78.6%;
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Pred. No. 62;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WEI, MING-Hui et al
HITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
HITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLE REFERENCE: CL001018
URRENT APPLICATION NUMBER: US/09/734,674
URRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(20200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                   CORRESPONDENCE
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APPLICANT:
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                            ZIP: 19406-0939
                                             COUNTRY:
                                                                                        STREET:
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                                                                                                      DDRESSEE:
                                                                                                                                             LICANT: Hodgson, John
LICANT: Knowles, David
LICANT: Knowles, David
LICANT: Stodola, Robert
LICANT: Stodola, Robert
LE OF INVENTION: No. 6348328el Compounds
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45, 649802
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                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 1355 base pairs nucleic acid
                                                                     King of Prussia
                                                                                                                                                                                                                                                                                                                                                   ATATAGAAGTCAAATGAACATCAGTTGA 170682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09734674
                                                         PΑ
                                                                                                                                                                                                                                                                       Application US/08858207A
                                                                                        709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                     SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202001)
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                                                                                                                                                                                                                            Michael
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Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.4; DB 4;
Pred. No. 1.6e+02;
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US-07-792-865D-1
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                              PILING DAIL.

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/01849
PILING DATE: April 3, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, Arthur
REGISTRATION NUMBER: 34,354
REFERENCE/DOCKST NUMBER: 5986/14692
PREFERENCE/DOCKST NUMBER: 577700
PROTEDHONE: (212) 527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 1, Application US/07792865D Patent No. 5646247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2179 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
TELEFAX: (212) 753-6237 FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19911004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MEROZOITE ANTIGENS LOCALIZED AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                            COMPUTER: IBM or IBM OPERATING SYSTEM: PC SOFTWARE: Wordperfec
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                            805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           John W. B
Samuel P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                           IBM or IBM-
                                                                                                                                                                                                                                                                                                                                                                                                                            Darby & Darby P.C.
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                                                                                                                                                                                                                                                                                                              Diskette,
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                                                                                5986/14692-US2
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Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                            inch,
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                                                                                                                                                                                                                                                                                                              360 Kb storage
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TOPOLOGY: STRANDEDNESS: LENGTH:

linear

NUCLEIC ACI

double

3763 base pairs

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                                                                                                                                                          Sequence 129, Application US/08961527
Patent No. 6420135
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                GENERAL INFORMATION:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: Lambda gt 11 na
LIBRARY: DNA expression
                                                                                            CORRESPONDENCE ADDRESS:
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CHROMOSOME/SEGMENT:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: Genomic DNA DESCRIPTION:
                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                    PPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP POSITION:
                                                                 STREET:
                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANELLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE:
                                                                              DDRESSEE:
                                                                                                                                                                                                                                           971 ATATAGAAGACGCÁGAAAAACAAGCT 996
               20850
                                                    Rockville
                                                                                                                                                                                                                                                                     ATATAGAAGCCCAAGAAAAATCAGCT 26
                                       Maryland
                                                               B: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                  Streptococcus pneumoniae Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                           80.8%;
                                                                                                          391
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Pred. No. 1.3e+02
0; Mismatches
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                                                                                                                                                                                                                                                                                           1.3e+02;
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                                                               Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/685,853A CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/182,194
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WEI, Ming-Hai et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                          NAME/KEY: misc feature
LOCATION: (1)...(74962)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL000871
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                             ENGTH: 74962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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 74050
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                              1 ATATAGAAGCCCAAGAAAATCAGCT 26
                                                               21;
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21; Conserv
                                                                                Similarity
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ATTTANGAGCCCATGAAAAGTCAGCT 74025
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                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                       2002-05-06
                                                                            60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.8%;
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                                                                              Score 18;
Pred. No.
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Pred. No.
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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1.5e+02;
                                                                                2.1e+02;
                                                                                               DB 4;
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                                                                                               Length 74962;
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                                                                Indels
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                                                               Gaps
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RESULT 15 US-09-671-317-387

Sequence 387, Application US/09671317

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ICCATION: 498.517
OTHER INFORMATION: 12-662-80.mis2, potential complement
NAME/KEY: primer_bind
LCCATION: 418..435
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LCCATION: 979..1000
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LCCATION: 485.509
OTHER INFORMATION: 12-662-80 potential probe
NAME/KEY: misc_feature
LOCATION: 24,726,739
OTHER INFORMATION: n=a, g, c or t
US-09-671-317-387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bougueleret, Lydie
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62.US3.CLP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR APPLICATION NUMBER: PCT/LB00/00403
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR PILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
Search completed: December 18, 2003, 09:04:15
Job time : 49.7705 secs
                                                                                                                                                                                                    Query Match 59.3
Best Local Similarity 75.5
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERTURE:
NAME/KEY: allele
LOCATION: 497
OTHER INFORMATION: 12-662-80 : polymorphic base G or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1000
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                                                                                                       971 ATGTAGAAGGACAAGAAAAAAGGTTGAC 999
                                                                                                                                            ATATAGAAGCCCAAGAAAATCAGCTGAC 29
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Chumakov, Ilya
                                                                                                                                                                                                                            59.3%; Score 17.8; DB 4; 75.9%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                       Length 1000;
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Result
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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        Score
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20.4
20.4
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Gapop 10.0 , Gapext 1.0
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1 atatagaagcccaagaaaaatcagctgacc
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      74.0
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/cgn2_6/ptodata/2/pubpna/US07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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17087
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6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
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6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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   10 US-09-070-927A-47
13 US-10-027-632-255052
14 US-10-027-632-255052
14 US-10-027-632-255052
15 US-09-880-107-2406
15 US-09-8817-30
15 US-10-084-817-30
16 US-09-918-995-36137
17 US-09-918-913-317-9
18 US-09-742-311-3
18 US-09-815-343-147079
18 US-10-027-632-147079
19 US-09-815-242-6699
10 US-09-070-927A-292
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Sequence 6797, Appl
Sequence 25052,
Sequence 255052,
Sequence 2406, Appl
Sequence 721, Appl
Sequence 30, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1379, Appl
Sequence 147079,
Sequence 6149, App
Sequence 6149, App
Sequence 6699, App
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US-09-815-242-6797

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Sequence 6797, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Chisen, Kari L.
APPLICANT: Ohisen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yamamoto, Robert T.
APPLICANT: NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/201,078
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259
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RESULT 3
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US-09-815-242-6797
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                                                                                                             Matches
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Best Local Similarity
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LOCATION: (1)
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APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 17987 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
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24; Conserv
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                          TAGAAGCCGAAGAAAATCAGTTGAAC 11301
                                                                         TAGAAGCCCAAGAAAAATCAGCTGACC 30
                                                                                                                                                                                                                                                                                                                                                     NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                     TELEPHONE: (301) 309-850
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDRESSEE: Human Genome Sciences, Inc.
                                                                                                          Conservative
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Dillon
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Pred. No. 3
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Pred. No. 2:
                                                                                                        Mismatches
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US-10-027-632-255052/c
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                                                                                    SOFTWARE: FastSEQ
SEQ ID NO 255052
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SEQ ID NO 255052
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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Best Local Similarity
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ORGANISM: Human
10-027-632-255052
                                                                                                                              PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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                                                                 ENGTH:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/185,218
FILLING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
                                                                                                                                                                                                 APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28
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Pred. No. 1
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                                                                PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR FILING DATE: 2000-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2406, Application Patent No. US20020142981A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/873,367C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10.
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                                                                                                                                                                                                                                                                                                                                                                                                          blication No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Genbank Accession No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                     ITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using ITLE OF INVENTION: Signature Gene Sets ILE REFERENCE: 689290-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ID NO 2406
ENGTH: 3610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION: Gene Expression Profiles in Liver Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/211,379
FILING DATE: 2000-06-14
APPLICATION NUMBER: US 60/237,054
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                                                      OF SEQ ID NOS: 1067
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Scherf, Uwe
Gene Logic, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          АТАGAAGCCCAAGAAAAATCAGCTGACC 30
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Ebner, Reinhard
                                                                                                                                                                                                                                                                                                                                        Endress, Gregory
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                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09873367C o. US20030165839A1
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                                                                                                                                                                                                                                                                                        Kenneth
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80.0%;
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82.1%;
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Pred. No. 2.2e
0; Mismatches
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Pred. No. 1.4e+02;
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2.2e+02
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Query Match
Best Local Similarity 84..
22; Conservative
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; ORGANISM: Homo sapiens
US-09-918-995-36137
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                                                                                                                                                                                                                                                                                                                                                     RESULT 8
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                                                                       CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRANKSEQ for Windows Version 3.0
SEQ ID NO 36137
                                                                                                                                                                                                                                                                                              Sequence 36137, Application US/09918995 Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PERL Program SEQ ID NO 30
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/270,784 PRIOR FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
                                                                                                                                                                                            APPLICANT: Hyseq, Inc.
FITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILE REFERENCE: 20411-756
FILE REFERENCE: 20411-756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030119009A1 1312325CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                       LENGTH:
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PPLICANT: Sharon E. Plon
PPLICANT: Jason M. Shohet
ITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
ILE REFERENCE: PA-0046 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3702
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                                                       405
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23; Conserv
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Pred. No.
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Pred. No. 2.2e
0; Mismatches
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2.2e+02;
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84.6%;

Score 19.6; Pred. No. 2

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Gaps

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; NAME/KEY: misc_feature
; LOCATION: (1): . (52354)
; OTHER INFORMATION: n = A,T,C or
US-09-742-311-3
                                                                                                                                        US-09-815-343-1379
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APPLICANT: GUEGLER, KAI' et al
APPLICANT: GUEGLER, KAI' et al
TITLE OF INVENTION: ISCLAIED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
                                                                                      Best Local Similarity
                                                                                                    Query Match
                                                                                                                                                                                                                                                                            SEQ ID NO 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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SEQ ID NO 3
LENGTH: 52354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1379, Application US/09815343
Patent No. US20010055596A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Patent No. US200
                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/742,311
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1)...(406)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                               ILE REFERENCE: 210121.504
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                                                                                                                                                                                                                                                                                                                                                                          TLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TLE OF INVENTION: DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYPE: DNA
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154 AAATACAAGTACCAGAAAAATAAGCTGAC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                  1 АТАТАGAAGCCCAAGAAAAATCAGCTGAC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, Jiangchun
                                                                    Conservative
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                                                                                  64.7%;
79.3%;
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                                                                Score 19.4; DB 9;
Pred. No. 2.7e+02;
0; Mismatches 6
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Pred. No. 5.2e+02;
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                                                                                               Length 406;
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RESULT 11

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; ORGANISM: Human US-10-027-632-147079
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; ORGANISM: Human
US-10-027-632-147079
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US-10-027-632-147079/c
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/195,218
                                                                                     PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASTSEQ for Windows Version 4
SEQ ID NO 147079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 147079, App. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 147079
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION. Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                            RIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                       FILING DATE: 1999-09-28
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                                                                                                                       for Windows Version 4.0
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Pred. No. 3
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RESULT 14
US-09-815-242-6699
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US-10-032-585-6149
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Best Local (
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                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITEA.011A CURRENT APPLICATION UNMERR: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
              PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/22,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
EQ ID NO 6149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Terry, Roes
APPLICANT: Bo, Jiang
                                                                                                                                                                                                                                                                              APPLICANT:
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LOCATION: (408)..(408)
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LOCATION: (408)..(408)
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APPLICATION NUMBER: 60/253,625
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Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                            Xu, H. Howard
                                                                                                                                                                                                                                                       Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                           Trawick, John D.
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87.5%;
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Pred. No. 3.
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US-09-070-927A-292/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6699
LENGTH: 2169
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Tocal Similarity
Tonserv
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                                                                                                     INFORMATION FOR SEQ ID NO: 292
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2169)
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                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1495 GAAGCCAAAGAAGAACAGCTGAC 1518
                                                                                                                                                               NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,3
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
SEQUENCE DESCRIPTION: SEQ ID NO: 292:
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
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Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GAAGCCCAAGAAAATCAGCTGAC 29
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                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                             LENGTH: 20561 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                          TELEFAX: (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven Barash
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Pred. No. 4.3e+02
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BER: PB369
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Search completed: December 18, 2003, 10:22:57 Job time : 968.902 secs	64.0%; Score 19.2; DB 87.5%; Pred. No. 6.4e+ vative 0; Mismatches GAAAATCAGCTGAC 29 	10; Length 2050 02; 3; Indels (561; 0; Gaps	0
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                    Match
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Gapop 10.0 , Gapext 1.0
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Copyright (a) 1993 - 2003 Compugen Ltd.
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gb_est2:*
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ALIGNMENTS

BE035293

MMM05C05 MM Mesembryanthemum crystallinum cDNA 5', mRNA sequence.

BE035293.1 GI:8330205

EST.

Mesembryanthemum crystallinum (common iceplant)

Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophylales; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 1086)

Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C.,

Scara, G., Wheeler, M. and Zepeda, G.R.

Functional Genomics of Plant Stress Tolerance

Unpublished

Contact: Michalowski, C.B.

University of Arizona

Bio Sciences West room 513, Tucson, AZ 85721, USA

Tel: 520-621-1982

Fax: 520-621-1982

Fax: 520-621-1982

Fax: 520-621-1981

Email: cbm@u.arizona.edu

Best blastz match: 'gi|1946367 (U93215) unknown protein

[Arabidopsis thaliana] 249 2e-65'. An open reading frame exists.

Insert Length: 1 Std Error: 0.00.

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  952032E05.y1 952 - BMS tissue
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Plate: 952032 row: E col
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                                                                                                           inote="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue, white selection on carbon collinearies and carbon collineary was size-fraction and carbon collineary was size-fractionally cloned and carbon collineary was size-fraction on carbon ca
                                                              carbenicillin-containing plates was used to recover positive clones."
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11 type="epidermal bladder cells"
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Plate: 1000086 row: G colu
Location/Qualifiers
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Stanford University
855 California Ave, Palo Alto, CA
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Fax: 650 725 8221
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 683
, 687, 707, and 945. Contigs were assembled using TIGR's
CAP program and a representative EST from each contig was
selected for the Unigene set. All singlets were also
selected."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="mRNA"
/db_xref="dbBST:606024G06.x2"
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Bukaryota;

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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                                                                                                                                              Email: walbot@stanford.edu
Plate: 1111017 row: B column:
Location/Qualifiers
                                                                                                                                                                                                                                                                                             Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304,
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/mol_type="mRNA"
/db_xref="dbEST:952032E05.y1"
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(tissue type="mixed"
(dev_stage="ear length from 0.5 cm - 2.0 cm"
(dev_stage="ear length from 0.5 cm - 2.0 cm"
(dev_stage="XLOIR (Stratagene)"
(clone_lib="606 - Ear tissue cDNA library from 1000 cm | 1000
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Brunus persica

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;

eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 645)
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Fax: 864 656 6879
Email: Aalbert@clemson.edu
Total High Quality bases = 603
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 645.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Abbott, A.
Dept of Genetics and Biochemistry
Clemson University
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nilarity 85.7%;
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                                                                                                                                                                                                                                                                                                /db_xref="taxon:3760"
/clone="pp_IEA0020M10f"
/tissue_type="Mesocarp"
/lab host="B. coli"
/clone_lib="Peach developing fruit mesocarp"
/clone_lib="Peach dev
                                                                                                                                                                   sequence analysis go to http://www.genome.clemson.edu/projects/peach. To order this clone go to http://www.genome.clemson.edu/orders* 107 c 165 g 184 t
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/note="This library represents the unique genes found in
the third round of RST sequences at Stanford University
for the maize genome project. Sequences are present from
library 952. Contigs were assembled using ZmDBAssembler
and 2 representatives from each contig were selected for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Unigene set. All singlets were also selected."
159 c 127 g 124 t
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Score 21.6; DB 13;
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0; Mismatches 4;
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RESULT 8
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TITLE
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                                                                             ORGANISM
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AY112254
AY112254.1
          Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org, ZmDB, www.radb.lastate.edu; TIGR, www.ncbi.nlm.nih.gov. When the source of t maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.lastate.edu.
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Zea mays
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Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                 SSS
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CC304082
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2 (bases 1 to 649)
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                                                                                                                                   CC304082.1 GI:30675523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="this sequence is part of a project of EST assemblies resulting from the application of wablic contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

131 g 172 t 25 others
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/db_xref="MaizeDB:633041"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
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/mol_type="mRNA"
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Seq primer: SP6
Class: BAC ends
                          Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

Research tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                 Unpublished
other GSSs: RPCII1-122J17.TV
other GSSs: RPCII1-122J17.TV
contact: Shaying Zhao, William Niero
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AGAAGCCCAAGAAAAATCAGCTG 27
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Gallus gallus BAC End
Unpublished
                                                                                                                                                                                                                                                                                                                                    Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
                                                                                                                                                                            Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                            Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
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Insert Length: 182000 Std Error: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Richard K. Wilson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Gallus gallus"
/mol type="genomic DNA"
/strain="Red Jungle Powl"
/db_xref="taxon:9031"
/clone="CH261-77A22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
a 192 c 129 g 313 t 2 others
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Catarrhini;
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                                                                                                                                                                                                                                                                               Mark Adams
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; Homo.
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RPCI-11-122J17,
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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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Best Local
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1 (bases 1 to 411)

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Relton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Relton,D., Brown,J., Kenty,G., Parmutt,A., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Cardenas

Schmitt,A., Theising,B., Role,R., Tsagareishvili,R., Williams,T.
                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
High quality sequence stop: ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bndocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_2: XhoI; cDNA made by oligo-dT priming.
NotI; Site_2: XhoI; cDNA made by oligo-dT priming ~1kb. 5'
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning. MD,
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Glone lib="REGI-11"
/note="Vector: pBACe3.6; Site_1;
RPCI11 Human Male BAC Library"
111 g 166 t
                                                                                                                                                                                         /tissue_type="Purified pancreatic islet"
/lab host="DH108"
                                                                                                                                                                                                                            /mol_type="mkNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127389"
                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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lib="RPCI-11"
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BASE COUNT
        77
314-362-1916, Fax: 314-747-2692."
3 125 c 46 q 163 +
                                   School of Medicine, Box 8127, 660 South Louis, MO 63110, E-mail: hinoue@imgate.v
                                                  Euclid
                                                  Ave.,
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끊 Ş Best Loc Matches Query Match Local 369 TATATAATCCTAAGGAAAAACAGCTGACC 24; Ŋ Similarity TATAGAAGCCCAAGAAAAATCAGCTGACC Conservative 70.0%; 0 Score 21; DB 13; Length 411; Pred. No. 1.4e+03; O; Mismatches 5; Indels 30 0 Gaps

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REFERENCE AUTHORS VERSION KEYWORDS SOURCE ORGANISM RESULT 11 BB048787/c COMMENT DEFINITION ACCESSION Scas 1 (bases 1 to 692)
1 (sarninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Arakawa, T., Carninci, P., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Mateuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

MIKEN Mouse ESTS (Arakawa, T., et al. 2001) BB048787 RIXEN full-length enriched Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus Mus musculus (house mouse) BB048787.2 BB048787 GI:15404011 enriched, Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus mRNA sequence. mRNA RNA linear EST 31-AUG-2001 adult male olfactory bulb Mus Mus.

Laboratory for Genome Exploration Research Group, Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (I 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa Tel: 81-45-503-9222
Fax: 81-45-503-9216 Unpublished On Jun 11, 2000 this sequence version replaced gi:8455935 Contact: Yoshihide Hayashizaki Research (RIKEN) Kanagawa RIKEN Genomic 230-0045, Japan

Email: genome-res@gsc.riken.go.jp,
URLihttp://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Maramatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), ra167-for rapid discovery of genes. Genome Res. 10 (10), ra167-for rapid discovery.
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Genome Res. Sugahara

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-89 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001)

further details. CDNA library was prepared and sequenced in Mouse Genome CDNA encyclopedia Project of Genome Exploration Research Gro Func. Genomics Please visit our web site (http://genome.gsc.riken.go.jp/)

Research Group in Riken

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COMMENT
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Best Local :
                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                          Srinivasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Raddatz, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A., Jesse, T., Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J. A. BAC-based genetic linkage map of the nematode Pristionchus
                                    Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chr
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                    genomic, genomic survey
BH833230
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                                                                                                           Contact: Sommer RJ
                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                             Pristionchus
                                                                                                                                                                                                                                                                                                            Pristionchus pacificus
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                     00497071601498
ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BamHI"
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dev_stage="adult"
lab_host="DH10B"
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strain="C57BL/6J"
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Pred. No. 1.5e+03;
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RESULT 13
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BMBAC318G10T7_PSU Brugia malayi Genomic Bac Library 3 Brugia malayi
genomic, genomic survey sequence.
BH761049
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Institute of Cell, Animal and Population Biology
University of Edinburgh
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1 (Dases 1 to 344)

Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Fost,J., Guillano,D., Slatko,B. and Blaxter,M.

Genome survey sequences from the human parasitic nematode Brugia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7 (TAATACGACTCACTATAGGG) Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit. The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +44 131 650 6760
Fax: +44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashworth Labs, King's Buildings, West Mains Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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                                                      /clone lib-Brugia malayi Genomic Bac Library 3"
/note-Tvector: pBACe3.6; Site_1: BamH I; Brugia malayi
/genomic DNA was partially cleaved with Sau3A I and size
fractionated. 7, 392 clones were generated with mean insert
size ~48 kbp. The library was constructed by Claire
whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
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/mol_type="genomic DNA"
/strain="var. California"
/db_xref="taxon:54126"
/clome_lib="Pristionchus pacificus BAC ends"
170 c 150 g 184 t
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                                                                                                                                                                                                                                                   /db xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/strain="TRS"
                                                                                                                                                                                                                                                                                                                                                               /organism="Brugia malayi"
/mol_type="genomic hwa"
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Score 20.6;
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1 (bases 1 to 730)

1 (bases 1 to 730)

1 Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished

Other_GSSs: BONEM78TR
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BONEM78TF BO 1.6 2 KB tot genomic survey sequence.
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1 (bases 1 to 498)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis
                                                           Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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CpG0718A CpIOWAGDNA1 Cryptosporidium
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DNA is from a doubled haploid provided by
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/clone_lib="BO_1.6_2_KB_tot"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
/note="Vector: pHOS1; Site_1: BstXI linkers"
total DNA inserted into pHOS1 using BstXI linkers"
215 c 114 g 291 t
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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Search completed: December 18, Job time : 1920.62 secs
                                                                                                                                                                                                                                                             BASE COUNT
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10717299
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For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seg primer: M13(-21) forward
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Tel: 415 206 8846
Fax: 415 206 3353
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Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
                                                                                                                                                                              Similarity
                                                                                 ATAAAGAAATTCAAGAAAATCTGCAGACC 466
                                                                                                                ATATAGAAGCCCAAGAAAAATCAGCTGACC 30
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                                                                                                                                                                                                                                                                                                                                                                                              parvum (1000) isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center (http://sequence-www.stanford.edu/group/techdev/shear.htm). The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small framework.
                                                                                                                                                                                                                                                                                             sephacryl S-400 to remove any small fragments and DNA eluting in the void volume was subcloned into an EcoR V-digested, alkaline phosphatase-treated pBlueScript II (SK-) vector and transformed into E. coli strain XL2 Blue MRF'. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and
                                                                                                                                                                                                                                                                              T7 primers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. coli XL2 Blue MRF'"
/clome lib="CpIOWAgDNA1"
/note="Vector: pBlueScript II (SK-); Site_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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strain="IOWA"
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80.0%;
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                    2003, 11:35:01
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Pred. No. 2.4e+03;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AUTHORS TITLE JOURNAL	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 AX028510 LOCUS DEFINITION		45		4 4 2 1		ພູພ ອີ			ωω ωα	32					c 23		20	19 19	17		145			9 69 6					بــر ر	Result
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predisposition WO 0042216-A 1	ens (human) ens ; Metazoa; Eutheria;	GI:10189693	from 1		15413	6881	9189	167	43804	43659	69272	26349 67108	06526	51900	22874	80236	22680	182527 67991	65842	53431	76364 35649	71901	87283	04454	09069	53954 69059	39873	95296	86491	35996	22706		Length 1
ition	7 C	18969	Patent															φφ 															D8
n 13 20-JUL-2000;	Chordata; Craniata; Ve: Primates; Catarrhini; I	33	30 bp DNA. 1t WOO042216.	ALIGNMENTS	AC135427	CHKCYSTAT	AX654979 AX251443	AC097832	AC136662	C128597	1016843	NS01RHA	1C104772	1096644	1C105481	3X248103	1133510	AL590115 AC006363	1C103866	1094604	1C126322 1C094592	C027240	1C022856	1E016956	C087856	11354862 1009514	C010612	\C120085	AC004810	1C096147	AC110652	X028510	ID
	Vertebrata; Buteleostomi; ; Hominidae; Homo.		linear PAT 16-SEP-2000		27 Oryza sa		AX6549/9 Sequence AX251443 Sequence		Rattus	Ratt.		Mus 1		Homo	AC105481 Rattus no	Danio	Human	AL590115 Human DNA AC006363 Homo sapi	Homo	Rattus	Homo Ratta		Homo	ACUZISEI HOMO SADI AE016956 Enterococ	NO TO	AL354862 Human DNA AC009514 Homo sapi	Homo s	Rattu	AC004810 Homo sapi	Rattus	AC110652 Rattus no	28510 Sequ	Description

AUTHORS

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                   AC110652.5 GI:25100613
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Matrix Biol. 14 (1), 31-40 (1994)
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1 (bases 1 to 2415)
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L24756.1 GI:438617
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Location/Qualifiers
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437 c
                                                                                                                                                                                                                                                                                                                                                                                                /map="Unassigned"
2179. .2260
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                  gene="BNSP"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 0.075;
); Mismatches
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Pred. No.
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(BNSP) gene, exon
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RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alden, J., Allen, J., Al
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TITLE JOURNAL REFERENCE AUTHORS

TITLE

JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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RESULT 4
AC096147
                            REFERENCE
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                                                          Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
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AC096147.6 GI:30522612
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                                                                                                                                                                                                                                                Rattus norvegicus clone CH230-10H14,
                                                     Rattus.
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NOTE: This is a 'working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length
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                         (bases 1 to 235996)
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Center clone name: CH220-83X21

Center clone name: CH220-83X21

Center clone name: CH220-83X21

Consensus program: Phrap; version 0.990329

Consensus quality: 214884 bases at least Q30

Consensus quality: 218820 bases at least Q30

Consensus quality: 218105 bases at least Q20

Estimated insert size; 221589; sum-of-contigs estimation.
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217264
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complement(195782..196630)
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44575 c 46422 g 62
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18001: gap of unknown length
217149: contig of 199148 bp in length
217249: gap of unknown length
221403: contig of 4154 bp in length
221503: gap of unknown length
222706: contig of 1203 bp in length.
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Hollins, B., Howells, S., Hladwin, S. L., Hodgson, A., Hogles, M.,
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Weinstock, G. and Gibbs, R.A.
Mailth, D.R., Holt, R.A., Smith, H.O.,
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24818200.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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Baldwin, D., Bandarnanike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Delgado, O., Denson, S., Dersmo, C., Ding, Y., Dinh, H., Divya, K.,
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Submithed (17-SEF-2001) Human Genome
of Molecular and Human Genetics, Bay-
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235996)
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                                                                   Rattus norvegicus clone CH230-304K12,
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Rattus norvegicus (Norway rat)
                                                                                                          AC131002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                   ACATAGAAGCCCATGAAAAATCAGCTG 46532
                                                                                                                                                                                                                                           ATATAGAAGCCCAAGAAAAATCAGCTG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                             67127
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------- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 224560 bases at least Q40
Consensus quality: 227267 bases at least Q20
Consensus quality: 227267 bases at least Q20
Consensus quality: 22867 bases at least Q20
Batimated insert size: 237036; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
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1 235996: contig of 235996 bp in length.
                                                                                                                                                                                                                                                                                Conservative
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clone_end:T7"
site:EcoRI
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complement(231640. .23
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clone_end:Sp6"
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clone_end:Sp6"
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47400 c 49017 g 66511 t
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|mol_type="genomic DNA"
|db_xref="taxon:10116"
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CARdenas, V., CATTER, K., CAVAZOS, I., CORRENT, S., Chen, E.,
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MANDENTIS, C., MARTINE, M., LEVAN, J., LAIS, L., KONTIS, S., LONGON, F., LONGOUCE, S., LODES, J.,
MARCHANA, S., MARTINE, M., MARTINE, J., MORTIS, S., MANTOLLON, M., MARTINE, S.,
MANDAR, S., MARTINE, J., MORTIS, S., MANTOLLON, M., MALLAND, M., MALLAND, M., MALLAND, M., MALLAND, M., MARTINE, S., MANTOLLON, M., MALLAND, Direct Submission
Submitted (08-CCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 19, 2002 this sequence version replaced gi:22267533.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Submitted (16-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Ada Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angui Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baldwin, D., Bandaranaike, D., Barber, M., Barnstee Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Rat Genome Sequencing Consortium. Direct Submission 2 (bases 1 to 266204)
Rat Genome Sequencing Consortium. Biswalo, K., Blair, J., Blankenburg, K., Blycn, F., Brown, Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B. Direct Submission (bases 1 to 266204) (bases 1 to 266204) Barber, M., bun, F Barnstead, M., Anguiano P., Brown, M., Adams, C Benahmed, F.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.hNOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 241240 bases at least Q40
Consensus quality: 244965 bases at least Q30
Consensus quality: 247564 bases at least Q30
Estimated insert size: 262891; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-304K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor Co
Center code: BCM
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/note="wgs_contig"
/n 50743 c 51682 g
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104571. .106534
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102208. .104470
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location,
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97500. .99912
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104570: gap of unknown length
256410: contig of 151840 bp in length
256510: gap of unknown length
257627: contig of 1117 bp in length
2577627: gap of unknown length
257781: contig of 1054 bp in length
258781: contig of 1054 bp in length
258881: gap of unknown length
260123: contig of 1242 bp in length
260123: gap of unknown length
261389: contig of 1166 bp in length
261389: gap of unknown length
261389: gap of unknown length
261389: gap of unknown length
262861: contig of 1166 bp in length
262861: contig of 116717 bp in length
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REFERENCE AUTHORS

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                                                                              Birren, B., Rasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boutwell, C.; Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Madconald, P., Marquis, N., McTris, W., Morris, W., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., O'Conmot, T., Favlin, B., Shyam, R., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome Y, Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 86491)

Birren,B., Fasman,K., Linton,L., Nusbaum,C., Page,D. and Lander,E. Homo sppiens chromosome Y, clone hCIT.69_H_8
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                                                                                              Zhao, J. and
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Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, B., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGrurk, A., McKernan, K., Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Machman, A., Nahf, R., Naylor, J., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Stange-Thomann, M., Stilwell, J., Stojanovic, M., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., 70, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Direct Submission
Submitted (08-UUR-1998) Whitehead Institute/MIT Center for Genome Submitted (08-UUR-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 86491)
Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatin,C., Boutwell,C., Brown,A., Castle,A., Cerny,J., Cooke,P., Depayre,E., Bevon,K., Dewar,K., Donelan,L., Etemadi,S., Ferreira,P.,

REFERENCE JOURNAL

Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, B., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Genshehmer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kamn, L., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Machman, A., Naylor, J., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Starickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Mannor, B., Warner, B., Wa Direct Submission
Submitted (27-JUN-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 86491)
Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatin,C.,
Baker,J., Baldwin,J., Castle,A., Cerny,J., Cooke,P., Depayre,B.,

Direct Submission

wagner, A.,

Wang, B.,

Wheeler, J., Wu, Y., Ye, W.J., Zhao, J.

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FEATURES
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Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boutwell, C., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreita, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gersigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Huil, J., Jacottot, L., Kann, L., Macdonald, P., Marquis, N., McKwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Macdman, A., Nahf, R., Naylor, J., O'Connoor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Skaletsky, H., Stange-Thomann, M., Stilwell, J., Stojanovic, N., Stone, C., Stickland, C., Subramanian, A., Sun, C., Torruella-Miller, I., Vassiliev, H., Voh, Wagner, A., Wang, B., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Only the last 86.5 kilobases of this clone are being submitted. The remainder overlaps accession number AC002531 (WICGR project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 27, 1998 this sequence version replaced gi:3253125. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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complement (5593. . 5819)
/xpt_family="MER20"
5830. . 5871
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complement(7886. .8
/rpt_family="Alusc"
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complement(6801..7104)
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complement(2526, .2824)
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105. .390
                                                                                  /rpt_family="Alusx"
7107. .7359
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zq88f03.s1"
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/db_xref="taxon:9606"
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RESULT 7 AC120085/c LOCUS DEFINITION

AC120085 195296 bp DN Rattus norvegicus clone CH230-490B8,

DNA linear 3, *** SEQUENCING

HTG 12-OCT-2002 IN PROGRESS

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77.3%; Score 23.2; DB 89.3%; Pred. NO. 36; vative 0; Mismatches CCAAGAAAATCAGCTGAC 29	complement (1565315831) /rpt_family="MER4_internal" complement (1583315965) /rpt_family="MER4_internal" complement (1597216220)	complement (1305 . 14587) /rpt family="Aluy" 14617 . 14912 /rpt family="Alusg" complement (14931 . 15353) /rpt family="MER4_internal" 15358 . 15647 /rpt family="Aluy"	complement(12659. 12966) /rpt_family="AluSp" complement(12967. 13508) /rpt_family="MER4_internal" complement(13486. 13986) /rpt_family="MER4_internal" family="MER4_internal" 13985. 14199 /rpt_family="LTR8" complement(14200. 14279)	20 = 20 20 H (1)	Eamily="Aludo" . 9314 . 9314 . 9314 . 9762 . 9762 . 9762 . 9762 . 10076 . 10076 . 1019 . 1023 . 10604 . 10604 . 10604 . 10604 . 10604 . 10604	AA224051, Ah224051, h"
9; Length 86491; 3; Indels 0; Gaps 0;				match to gi 1802573, clone match to gi 1802573, clone		match to gi 1844592, clone match to gi 1802456, clone

SOURCE

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AUTHORS
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                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Bacen, H.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Barbetead, M., Brahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, M., Bhaby, C., Burch, P., Burrell, K., Colderon, E.,
Chacko, J., Charez, K., Cavazos, I., Ceasar, H., Center, A., D.,
Chacko, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Chacko, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Claveland, C., Cockrell, R., Cox, C., Coyle, K., Cree, A., D. Souza, L.,
Davvla, M., L., Davvs, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Derman, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Duzbin, K., Duval, D., Eaves, K.,
Egan, A., Escotto, M., Engere, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C. M., Gabis, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Genbregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guerra, M.,
Gendrathe, P., Haeland, W., Handl, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlat, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgeon, A., Hogues, M.,
Hollins, B., Howells, S., Hillyk, S., Hume, J., Idlebird, D., Jackson, L., Jackson, L., Jackson, L., Jackson, L., Jackson, A., Jackson, L., Jackson, L., Jackson, L., Jackson, J., Jackson, A., Jackson, A., Lorassan, M., Wahindartne, M., Mahmoud, M., Malboy, K., Margum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Pal, S., Parks, K., Palse, C., Neal, N., Mcheod, M., Pats, R., Weits, R., Pats, 
Direct Submission
Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                Submitted (03-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 195296)
                                                                                                                                         Rat Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                   Worley, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allen, C., Allen, H., Alsbrooks, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ***, 5 unordered pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.lgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a "working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
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184880
188095
188195
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Assembly program: Phrap; version 0.990329
Consensus quality: 175959 bases at least Q40
Consensus quality: 178795 bases at least Q30
Consensus quality: 180615 bases at least Q30
Estimated insert size: 177042; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-490B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                    5152.
                                                                                                                                                                                                                                            end_sequence:RXBRP04TJ"
complement(167606. .168
179471. .180564
                                                                                                                                                                                                                                                                                                                                                                                                                           clone_end:
                         note="wgs_end_extension
lone_end:Sp6"
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:lone end:T7"
                                                                                    nd_sequence:RXBRP04TV"
73865. .177056
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lone end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
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184879: gap of unknown length
184894: contig of 3215 bp in length
188194: gap of unknown length
191782: contig of 3588 bp in length
191882: gap of unknown length
191200: contig of 1318 bp in length
193300: gap of unknown length
193300: gap of unknown length
193300: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="genomic DNA'
xref="taxon:10116"
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It currently
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/note="wgs_end_extension clone_end:Sp6"

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REFERENCE
AUTHORS
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                                                                                                    SOURCE
ORGANISM
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ORIGIN
 REFERENCE
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AX695617/c
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                                                                                                                                    KEYWORDS
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                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                                                                                                         3 ATAGAAGCCCAAGAAAAATCAGCTGAC 29
                                                                                                                                                                                                                                                                                                                                   24:
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebzata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 139973)

DOB Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sagres Discovery (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX695617.1 GI:29418769
            Unpublished
                             Direct
                                                                                                     Homo sapiens
                                                                                                                  Homo sapiens (human)
                                                                                                                                    HIG
                                                                                                                                                 AC010612.8 GI:14971174
                                                                                                                                                                                Homo sapiens chromosome 5 clone CTB-91C24, complete
                                                                                                                                                                                                AC010612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris, D.W. and Engelhard, S.K.
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Homo sapiens
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(bases 1 to 139873)
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                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compositions and methods for cancer: WO 03008583-A 1244 30-JAN-2003;
                             Submission
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/note="wgs_end_extension
clone_end:Sp6"
a 41149 c 42292 g 48361 t
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182511. .184779
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                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
20559 c 21158 g 26915 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DN;
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .96595
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Pred. No. 9
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
AL354862
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                                                                        Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1sA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 29, 2001 this sequence version replaced gi:16501113. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation amoutation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
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Estimated Total Number of Errors is 0.4.
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On Jul 20, 2001 this sequence version replaced gi:14277265.
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Submitted (16-8EP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USJ (bases 1 to 139873)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Human DNA sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 (bases 1 to 139873)
DOS Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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Pred. No. 94;
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xm clone RP11-83L6 on chromosome
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Submitted (25-AUG-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                         2 (bases 1 to 169059)
Bruno, D., Conn, L., Dela Rosa, M.,
Glukhov, S., Hansen, N., Hyman, R.,
Ramirez, D. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 169059)
Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J.
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                                                                                                    Direct Submission
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RPII-83L6 is from the library RPGI-11.1 constructed by the group of Pieter de Jong, For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iomo sapiens (human)
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/note="Sequence from overlapping clone RP11-148I22 (AL162585). Assembly confirmed by restriction digestranged in the confirmation of the confirmation of
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mol_type="genomic DNA"
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                                                                                                                                                     Federspiel, N., Foreman, P., Mao, J., Morehouse, A.J., Oefner, P.,
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Homo sapiens chromosome 8, clone RP11-4K16
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/db_xref="taxon:9606"
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Location/Qualifiers
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mol_type="genomic DNA"
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PEATURES SOURCE	COMMENT	JOURNAL	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
Location/Qualifiers 1. 169060 /organisms"Homo sapiens" /mol_type="genomic DNA" /db_xref="texcon:9606" /chromosme="8" /chrome="8" /clone="RP11-4K16" /clone_lib="RPCI-11 Human Male BAC"	version replaced gi:2 slig RepeatMasker: 6-1997) edu/RM/RepeatMasker.ht te/ MIT Center for Ger te/ mit.edu wi.mit.edu ations@genome.wi.mit.edu ation	B., Choepel, Y., Collymore, A., J. Choepel, Y., Collymore, A., J. M., Gage, D., Galagan, J., Grand-Pierre, N., Hafez, N., Iliev, I., Johnson, R., Jones, C. Landers, T., Levine, R., Landers, T., Levine, R., Landers, T., Levine, R., Johnson, R., Jones, C. Landers, T., Levine, R., Johnson, R., Major, J., Min, J., Meneus, L., Mihova, T., Nguyen, C., Nicol, R., Norbu, Ce, N., Retta, R., Nguyen, C., Neil, D., Oliver, J., Lell, P., O'Neil, D., Oliver, J., re, N., Raymond, C., Retta, R., Y.A., Schauer, S., Schuyback, R., Y.A., Schauer, S., Schuyback, R., Spencer, B., Stange-Thomann, N., Spencer, B., Stange-Thomann, N., ye, S., Theodore, J., Topham, K. 3, Vo, A., Wilson, B., Wi, X., Zembek, L., Zimmer, A., and Zody ad Institute/MIT Center for Ge	ke, P., DeArellano, K redira, P., FitzGerala Sord, S., Graham, L., rton, L., Hulme, W., rtatas, A., Kella, C., K., Liu, G., MacLean McCarthy, M., Meldra McCarthy, M., Meldra McCarthy, P., Pierr McCarthy, P., Pierr Mry, P., Roman, J., Pest Phunkhang, P., Pierr Mry, P., Roman, J., Test Savery, P., Smith, C., Talamas, J., Test Massiliev, H., Viel, I Mng, G., Zainoun, J., saion Charles Street, Ct o 169060)	., Subram ., Travis . Wu,X., I . Zimmer, . Zimmer, . Dmission . (01-PEB- . 320 Char . 1 to 169 . Nusbaum, . Nusbaum, . Bastien, V
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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Homo sapiens chromosome 17, clone RPI1-956N15, complete sequence.
AC021581
AC021581.10 GI:18104877
                                                                             Submitted (16-JAN-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 181607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C. and Lander,B. Homo sapiens chromosome 17, clone RP11-956N15 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ATAGAAGCCCAAGAAAAATCAGCTGAC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAGAAACTCAAGTAAAATCAGCTGAC 116085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nmalia; Butheria; Pr
(bases 1 to 181607)
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/note="<30 qual SNG1 region."

complement (40628...40634)

/note="<30 qual SNGL region."

/note="<30 qual SNGL region."
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complement(40131. .
/rpt_family="MBR94"
                                                                                                                                                                                       and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="<30 qual SNGL region."
complement(40726. .40793)
/note="<30 qual SNGL region."
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/note="<30 qual SNGL region."
complement(40704. .40708)</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="MSTA-int"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="<30 qual SNGL region."
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88.9%;
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ement (4000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="MSTA-int"
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family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="MSTA"
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Pred. No. 93;
0; Mismatches
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                                                                                                                                for Genome
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COMMENT JOURNAL

FEATURES

only

submitting the middle 181607 bps of the clone [111208 = unique]. Location/Qualifiers

and ACO21582 (WICGR project 15758) at the T7 end by 81850 bps. We

overlaps AC021580 (WICGR project 15756) at the SP6 end by

source

1. .181607

/organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606" /chromosome="17"

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Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitchigh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Govd, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heafcod, A., Horton, L., Hilme, M., Lievin, R., Miu, G., McCarthy, M., Kamat, A., Kartas, A., Kells, C., Lankacres, R., Landers, T., Leoccky, J., Levine, R., Miu, G., McCarthy, M., McCarth
                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 10, 2002 this sequence version replaced gi:15487420. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                             Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L5757
Center clone name: 956_N_1
                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
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REFERENCE

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/rpt_family="MLTIG1"
20583. .20603
                                                                                                    complement (18320.
                                                                                                                                                            complement (17578, .17868)
                                                                                                                                                                                                                                                                                                                                                                                                           complement (13589. .14719)
/rpt_family="L1M2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (13293, .13618)
/rpt_family="L1M1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
complement(2668. .294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (736. .1025)
/rpt_family="Aludb"
  /rpt_family="AT_rich"
                                                                                                                                             complement (18015.
                                                                                                                                                                                                         complement(15581, .17070)
/rpt_family="L1M2"
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Total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "rpt_family="(TG)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _family="AluY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _family="LTR9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="MER34"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="AluSx"
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                                                                                                  family="AluSx"
ement(1927)
                                                                                                                                                                                                                                              _family="(TATATG)n"
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                                                                family="11M4c"
. . 19060
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ement (1222)
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                                                                                                                                                                                                                                                                                                                           family="(TATATG)n"
                                                                                                                                                                                                                                                                                                                                                                  family="L1MCa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="MER51B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="AluSx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="L1MB3"
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AE016956/c
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                                                                                                                                                                                                       Direct Submission
Submitted (03-FZB-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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Paulsen, I., Banerjei, L., Myers, G.S.A., Nelson, K.E., Seshadri, R., Read, T.D., Fouts, D.B., Eisen, J.A., Gill, S.R., Heidelberg, J.F., Read, T.D., Fouts, D.J., Umayyam, L., Brinkac, L., Beanan, M., Tettelin, H., Dodson, R.J., Umayyam, L., Brinkac, L., Beanan, M., Daugherty, S., DeBoy, R.T., Durkin, S., Kolonay, J., Madupu, R., Nelson, W., Vamathevan, J., Tran, B., Upton, J., Hansen, T., Shetty, J., Khouri, H., Utterback, T., Radune, D., Ketchum, K.A., Dougherty, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE016956 304454 bp DNA linear BCT 28-Washerococcus faecalis V583, section 10 of 11 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Fraser, C.M.

Role of Mobile DNA in the Evolution of Vancomycin-Resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                        and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis
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/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (24479...24593)
/rpt_family="AluJo"
complement (24666...24713)
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complement(94...2529)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(TATG)n"
complement(23398. .23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family=".
22874. .23032
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                                                                                                                                           /organism="Enterococcus faecalis V583"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="L1M4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 22.2; D; pred. No. 92; O; Mismatches
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BGEIATIGBHTAEI GVSTGTDWTRDYSQSGALRSJLGTVSTEKQGLPABEVDEYLKK
GYARNDRVGTSYLEKQYEDYLQSKKAKSEVVLDNIGKI VSQTPISKCEKGSINIKLTID
SNFQNKYDEILQRNYSQI VKTIGPYSENAYVYANNPQYGAILAMSGPHIDLAGTGVTF
NPLAPILINSEVPGSVVKAGTLTAGYETGVI KCHDVLTDEAILLAGSREKASIWNNASGG
TTMQLTAEQALEYS SNAYMKL VFKOMGVNYYPIMI FPYEVGDDTVFKELRKAFAEYG
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NQQIIADVEAGKGNYQYNAKDFYKAPBITKEDQTLKATLTTLANKLNKTITVDINGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYYDTDNGESPYTAEDLPAIBAEMKI VKENNPIVRKEISRAEALELFADDPYKVELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVEDLSIFIDSMAAEVHNYSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIVRLGYLQIVEGEEFNKKITANSSLQITTPSPRGQIYDSQGKVLVSNKANLAITYTR
GKNIEGKDILFIANKVNELINVPVDPNLTDRDKKDYWLANPENLKAAQSKLTDQDKED
EKGNKITDECTLYAKAVEKVIPBEIAFDDRTLQAVTIFKRMNAASQMVIVFIKNEGVT
                                                                                                                                                                                                                                                                                                                                                                                                       complement (5072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (5072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELKKDRYAQGGEWKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCEHHMMYZKODIKSYRELPIRIABLGMMKRYEKSGALSGLQRVREMTLINDGHTFVRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (2394. .4331)
VAFDKTQIQNVLNDDGTINKEKLTTWVTQLETTYGSANQPVLFTDVHGTTRRFKNNGS
                                                                                                                                                                     /transT table=11
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protein_id="AAO82552.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KERLQAQGLRVEVDDRNEKMGYKIRASQTQKVPYQLVVGDKEMEDATVNVRRYGSKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIDLDRPIVEDGSLEIVTPDHEDALGILRHSSAHLMANALRRLFPNIKFGVGPAIDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cranslation="MKKNSFIDKIKKTDAAAKSQRGRKPHIPFRLNLLFFVIFTLFVS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MSIHITFPDGAVKPFDSGITTFDVAKSISNSLAKKALAGKFNGV
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                                                                                                                                                                                                                                                                                                                                                                           _tag="EF2860"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             table=11
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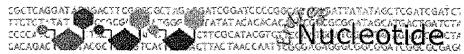
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVYIVEPCAEFFETATWIAKFGQPLIMQRPKEMTLFPTBPKTRETFLMLFEDGQRIDL
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complement (10676.
                              enndtnlgflgmngndfffraqskomaanggtgtvgffrvspogavritdargn"
                                                                                                                                                                                                                                                                                                                                                                                                                 complement (9611
                                                                                                                                                                                                                                                                                                                                                                                                                    locus_tag="EF2864"
complement/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (6664. .7527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIYGHIYDDAPGEFDKPVDYGEEV"
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protein_id="AAO82555.1"
db_xref="GI:29344798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transī
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="EF2862"
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protein_id="AAO82553.1"
db_xref="G1:29344796"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus_tag="EF2861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="aadK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MGHQLSTHFFNKKTGIISTFLSLILLVGGLLFALPAFEVQAAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="conserved h
protein_id="AA082554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MRTESEMFQLIMDVAKQESHIRAVGMVGSRTNVKAPKDSFQDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
transl_table
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   .11395)
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54.1"
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Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Boo
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		Limits	Preview	Index	History	Clipbo	ard D	etails
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☐ 1: AX028511. Sequence 14 from ...[gi:10189694]

Links

LOCUS AX028511 31 bp DNA linear PAT 16-SEP-2000

DEFINITION Sequence 14 from Patent W00042216.

ACCESSION AX028511

VERSION AX028511.1 GI:10189694

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Kusk, P.

TITLE Genetic predisposition

JOURNAL Patent: WO 0042216-A 14 20-JUL-2000;

OSTEOMETER BIOTECH AS (DK) ; KUSK PHILIP (DK)

FEATURES Location/Qualifiers

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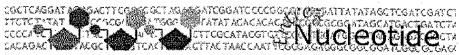
Disclaimer | Write to the Help Desk NCBI | NLM | NIH

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Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Воо
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Links

LOCUS AX028510 30 bp DNA linear PAT 16-SEP-2000

DEFINITION Sequence 13 from Patent WO0042216.

ACCESSION AX028510

VERSION AX028510.1 GI:10189693

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Kusk, P.

TITLE

Genetic predisposition JOURNAL

Patent: WO 0042216-A 13 20-JUL-2000;

OSTEOMETER BIOTECH AS (DK) ; KUSK PHILIP (DK)

FEATURES Location/Qualifiers

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ORIGIN

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